OM protein - protein search, using sw model

6, 2004, 16:20:48 ; Search time 25.2632 Seconds (without alignments) 55.921 Million cell updates/sec October Run on:

US-09-635-974A-2 31

1 NYGVH 5 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A Geneseq 29Jan04:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

Description	Aaw08938 CDR1 from	Aay59311 Heavy cha	٠.	Aau77784 Mouse hea	Abo32615 Secreted	9	Aaw05823 Humanised	Aag33864 Arabidops	53	Aaw08950 Heavy cha	Aaw08952 Heavy cha	Aaw08951 Heavy cha	Heavy	Aay90818 260F9 hyb	Human	Aaw08947 Heavy cha	4	42	Aay79257 Putative	78	Abo32630 Secreted	Aay79267 Mouse put	77 Murine	5622	Aae37329 Human VLC
B ID	<		4 AAB37952	5 AAU77784	6 ABO32615	4 AAM93396	2 AAW05823	3 AAG33864	2 AAW08953	2 AAW08950	2 AAW08952	2 AAW08951		3 AAY90818	3 AAB00210	2 AAW08947				4 AAU00478	6 ABO32630	3 AAY79267	4 AAU00477		6 AAE37329
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AAW29676 ABO32609 AAR032609 AAR02191 AAW02133 AAW03134 AAR06483 AAR3680 AAR09650 AAR99649 AAR99648 AAW3192 AAR39648 AAW3192	AAG79838 ABO32607
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	-
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	31
01000000000000000000000000000000000000	44 45

ALIGNMENTS

RESULT 1

Complementarity determining region 1; CDR1; heavy chain; variable region; reshaped; human, monoclonal; antibody; H225; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate. CDR1 from heavy chain variable region of reshaped H225 antibody. Ā. AAW08938 standard; peptide; 5 (first entry) 18-SEP-1997 AAW08938; AAW08938

Homo sapiens.

WO9640210-A1.

19-DEC-1996.

96WO-US009847. 07-JUN-1996; 95US-00482982. 95US-00573289. 07-JUN-1995; 15-DEC-1995;

(IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.

Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;

WPI; 1997-051897/05.

- nseq Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.

Claim 1, Page 83; 112pp; English.

The present peptide is the complementarity determining region 1 (CDR1) from the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour calls, especially late stage prostatic tumour cells in humans, optionally conjugated a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, rals cycle inhibitor

Sequence 5 AA;

Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.

99US-00312284. 99US-00374028.

14-MAY-1999; 13-AUG-1999;

01-MAY-2000; 2000WO-US011756.

WO200069459-Al.

ds sny

23-NOV-2000.

Anti-EGFR monoclonal antibody H chain V region CDR1 peptide sequence.

(first entry)

12-MAR-2001

AAB37952 standard; protein; 5 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the hypervariable region CDR1 (complementarity determining region 1) of the heavy chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to the patient makes the tumour more susceptible to radiotherapy
                                                                                                                                                                                                              Hypervariable region; complementarity determining region; CDR; tumour; single chain antibody; growth inhibitor; human; tumourigenesis; therapy; protein receptor tyrosine kinase; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.
                              Gaps
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       / Match 100.0%; Score 31; DB 2; Length 5; Local Similarity 100.0%; Pred. No. 1.40+06; nes 5; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                          Heavy chain hypervariable region, CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Robert F,
                                                                                                                          AAY59311 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                           98US-00079612.
98US-0085613P.
98US-00206138.
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                                                                                                                                                                                                                                                                                                                                                                                     (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND.
                                                                                                                                                                     07-MAR-2000 (first entry)
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Best Local Similarity 1000.
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                                                                   1 NYGVH
                                                   NYGVH
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15-MAY-1998;
07-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Waksal HW,
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          Query Match
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Matches
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                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                               Disclosure; Page 13; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU77784 standard; peptide; 5 AA.
(IMCL-) IMCLONE SYSTEMS INC
                                                                                                   WPI; 2001-016160/02.
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                                                 Waksal HW;
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RESULT 3 AAB37952

US2003022279-A1.

30-JAN-2003

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                     of a member of the EGF receptor family, or a combination of the antiagonist and photocherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal growth factor receptor (EGFR) antagonist by inhibiting EGFR /HERI phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic keratoses, seborrheic keratoses, warts, keloid scars and eczema similated by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 255 antibody heavy chain (VH) hypervariable region (CDRI) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, TANGO, INTERCEPT, secreted polypeptide; immune disorder;
hormonal disorder; proliferative disorder; cancer; thyroid disorder;
diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
myocardial infarction; congestive heart disease; blood platelet disorder;
thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
                                                                                                                                                                                                                                                             Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGF) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR1; EGFR inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 5; Length 5; ilarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted polypeptide-related peptide #42.
                                                                                                                                                                                                                                                                                                                Disclosure; Page 11; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO32615 standard; peptide; 19 AA.
                                                                                                                          09-AUG-2001; 2001WO-US041647
                                                                                                                                                  09-AUG-2000; 2000US-00635974.
                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                         WPI; 2002-257423/30.
N-PSDB; ABK11440.
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Best Local Similarity
Local 5; Conserv?
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                                                                         WO200211677-A2
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The invention relates to secreted polypeptide-related proteins and nucleic acids (TANO) and INTERCEPT proteins and nucleic acids). The nucleic acids, proteins and antibodies specific to the proteins are uncleic acids, proteins and antibodies specific to the proteins are useful in screening assays, predictive medicine (e.g. diagnostic assays, prophostic assays, monitoring clinical trials and pharmacogenetics) and diagnosing, preventing or treating proliferative disorders (e.g. andithiple sclerosis or lupus), neurological disorders (e.g. multiple sclerosis or lupus), neurological disorders (e.g. multiple sclerosis or lupus), neurological disorders (e.g. proporters (e.g. multiple sclerosis or lupus), neurological disorders (e.g. proteiner's disease or Parkinson's disease), cardiovascular disorders (e.g. proteiner's disease or Parkinson's disease), cardiovascular conferente disorders (e.g. thromboyycopenia or ansemia) and disorders involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic acids may also be used in chromosome mapping, tissue typing and forensic polypeptide-related peptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from USPTO at conferent processed the processed that a secreted conference in the patent of the conference o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202, TANGO 201, TANGO 201 or INTERCEPT 217), useful for diagnosing, preventing or treating disorders such as cancer, diabetes or atherosclerosis, and in forensic biology.
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Mccarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
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                                                                                                            99US-00342364.
99US-00393996.
99US-00420707.
                                                                                                                                                                                                                                                                                                                                          16-JUN-2000; 2000US-00596194.
23-JUN-2000; 2000US-00602871.
30-JUN-2000; 2000US-00608452.
                                                                                                                                                                                                                             2000US-00479249.
2000US-00559497.
2000US-00578063.
12-JAN-2001; 2001US-00759130
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nes 5; Conservative
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GOODEARL A D J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRASER C C.
BARNES T M.
SHARP J D.
KIRST B J.
MYERS P S.
LEIEFY R R.
HOLIZMAN D A.
WRIGHTON N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-456290/43.
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                                                                                                                                                                                                                             07-JAN-2000; 27-APR-2000; 24-MAY-2000; 2
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                                                                                                                                                 10-SEP-1999
                                                                            14-JUN-1999
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(MACK/) 1
(GOOD/) 0
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(BARN/)
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(MYER/)
(LEIB/)
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NYGVH 10

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/note= "human framework residue 82 is substd. by a consensus amino acid of the equivalent murine framework residue"
                                                                       /note= "human framework residue 27 is substd. by
equivalent murine framework residue"
29
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equivalent murine framework residue"
30
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equivalent murine framework residue"
Misc-difference 73
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equivalent murine framework residue"
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equivalent murine framework residue"
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equivalent murine framework residue"
Misc-difference 78
                                                                                                                                                                                          /note= "human framework residue 30 is substd. equivalent murine framework residue"
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(IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Link BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Fig 4b; 85pp; English.
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/label= CDR1
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/label= CDR2
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/label= CDR3
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 Homo; sapiens.
Mus sp.
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                                  Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for Synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-cell lymphoma; humanised antibody; bispecific antibody; myeloma; leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                        Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 2992; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 4; Length 107; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping.
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   Ā
                                                                                              Human polypeptide, SEQ ID NO: 2992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW05823 standard; protein; 116 AA.
AAM93396 standard; protein; 107
                                                                                                                                                                                                                                                                                        08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                                           07-JUL-2000; 2000EP-00114089.
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                                                             (first entry)
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in genetic manipulation.
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27-JAN-1997 (first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAK94317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 AA;
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                              EP1130094-A2
                                                               06-NOV-2001
                                                                                                                                                                                                                            05-SEP-2001
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                                AAM93396
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The variable region (AAW05823) of the humanised IDIO antibody heavy chain (AAW05829) consists of human IC4 heavy chain variable region framework (substd. at 9 positions with mouse or consensus human amino acids) and complementarity determining regions from the murine IDIO antibody specific for a 28/32 kDa heterodimeric antigen present on the surface of malignant B-cells. It can be coexpressed with humanised IDIO light chain (see also AAW05828) in e.g. mouse myelome NSO cells. Humanised antibody fragments can be incorporated into novel bispecific antibodies reactive Wath both effector cell antigens (see also AAW05820) and malignant B-cells. (Updated on 16-OCT-2003 to standardise OS field)
New bi-specific antibody reactive with both T or NK cells and malignant scells - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia, lymphoma and myeloma.
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RESULT 7 AAW05823

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9904S-0138840P-9904S-01388447P-9904S-01388447P-9904S-01388447P-9904S-01388447P-9904S-0138447P-9904S-01394452P-9904S-01394452P-9904S-01394452P-9904S-01394452P-9904S-01394452P-9904S-01394452P-9904S-0142947P-9904S-0142332P-9904S-0142332P-9904S-0142332P-9904S-0142332P-9904S-01443332P-9904S-01443332P-9904S-01443332P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-01443333P-9904S-0145919P-9904S-0145919P-9904S-0145919P-9904S-0145919P-9904S-0145919P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144392P-9904S-0144494
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                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                              Gaps
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0
                      Length 116;
                                             0; Indels
                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 41114.
                      Cuery Match 100.0%; Score 31; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                               AAG33864 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                     99US-0121825P

99US-0123180P

99US-0125788P

99US-0126264P

99US-0126264P

99US-0126264P

99US-0128244F

99US-0128244F

99US-013093P

99US-013093P

99US-0130891P

99US-0130891P

99US-0131449P

99US-0131449P

99US-0131448P

99US-0131448P

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99US-0131448P

99US-0131448P

99US-0131448P

99US-013144P

99US-013148P

99US-013141P

99US-0134218P

99US-013422P

99US-013478P

99US-0135124P

99US-0135124P

99US-0135124P

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99US-0135124P

99US-0135124P
                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                          18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                    31 NYGVH 35
                                                                  1 NYGVH 5
  Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                       25-FBB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
06-APR-1999;
06-APR-1999;
10-APR-1999;
10-APR-1999;
10-APR-1999;
30-APR-1999;
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                                                                                                                                                                    AAG33864;
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AAG33864
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The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) #225, 225RHD. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                         Heavy chain; reshaped, monoclonal; antibody; 225RD; human; eppldermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 2; Length 119; 100.0%; Pred. No. 1.2e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW;
                                                                                                                      Heavy chain variable region of 225RD antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                         31. .35

/label= CDR_1

/label= Framework_2

50. .65

6. .97

/label= CDR_2

/label= Framework_3
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/label= framework_1
                                                            AAW08953 standard; protein; 119 AA.
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/label= C
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Best Local Similarity
Matches 5; Conserv
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NYGVH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 119 AA;
                                                                                                    18-SEP-1997
                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
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15-DEC-1995;
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                                                                              AAW08953;
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99US-014972P

99US-014972P

99US-014972P

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99US-014973P

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99US-0151080P

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9903-0169741P
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9903-0160980P
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99US-0162142P.
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99US-0159294P.
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Best Local Similarity
Matches 5; Conserv
 09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
16-AUG-1999;
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26-OCT-1999;
28-OCT-1999;
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1 NYGVH 5

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Heavy chain; reshaped; monoclonal; antibody; 225RC; human; epidérmal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                Heavy chain variable region of 225RC antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldstein NI, Giorgio NA, Jones ST,
                                                     standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
  NYGVH 35
                                                                                            18-SEP-1997
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          WO9640210-A1
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15-DEC-1995;
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                                                                        AAW08952;
   31
                                                    AAW08952
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Region
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                                          AAW08952
                                                              Heavy chain, reshaped, monoclonal, antibody, 225RA, human, epidermal growth factor; BGF, receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostatic, variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H255, 225RH. The MAD is specific for the human monoclonal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage agent tumour calls in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 2; Length 119; llarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giorgio NA, Jones ST, Saldanha JW;
                                                                                                            Heavy chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                              50. .65
/label= CDR_2
66. .97
/label= framework_3
                                                                                                                                                                                                                   1. .30
/label= framework_1
31. .35
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/label= framework_4
                                                                                                                                                                                                         Location/Qualifiers
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                                                  AAW08950 standard; protein; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                   98. .108
/label= CDR_3
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95US-00573289.
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                                                                                          (first entry)
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31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein NI,
                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
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15-DEC-1995;
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                                                                      AAW08950;
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                                          AAW08950
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1. 30 /label= framework_1 31. 35 /label= CDR_1 36. 49 /label= framework_2 /label= CDR_2 /label= CDR_2 /label= CDR_2

95US-00482982. 96WO-US009847

18. .108 /label= CDR_3

Location/Qualifiers

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                                                                                                                             Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
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Saldanha JW;
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                                                                  WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Query Match

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31 NYGVH 35

(first entry)

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Heavy chain variable region of 225RE antibody.
                                                    AAW08954 standard; protein; 119
                                                                                        18-SEP-1997
                                                                      AAW08954;
                                   RESULT 13
                                            AAW0895
                                                               Heavy chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHB. The MAD is specific for the human monoclonal prowth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 31; DB 2; Length 119; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saldanha JW;
                                                                                                          Heavy chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                      36. 49
/label= framework_2
50. 65
/label= CDR_2
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                                                                                                                                                                                                                                                                                                             109. .119 __/label= framework_4
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/label= framework_1
                                                      AAW08951 standard; protein; 119 AA.
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 30; Fig 22; 112pp; English.
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31 NYGVH 35
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                                                                       AAW08951;
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                        tumour; cell;
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Heavy chain, reshaped, monoclonal, antibody; 225RE; human, apidermal growth factor; EGF; receptor; inhibition; growth, late stage; prostatic, prostate, variable region; framework; complementarity determining region; CDR.
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100.0%; Pred. No. 1.2e+02;
cive 0; Mismatches 0; Indels
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/label= CDR_2
66. .97
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/label= framework_2
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label= framework_1
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                                                                                                              Homo sapiens.
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The present invention describes a monoclonal antibody (MAb) (I) that binds to a human breast cancer antigen that is also bound by MAb 454C11 and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also described is a hybridoma that produces (I). (I) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence represents a VH domain derived from a 260F9 hybridoma, which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                      Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma; specific binding assay; affinity purification; drug targeting; toxin targeting; imaging; genetic; therapeutic.
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                                                                                           260F9 hybridoma VL domain SEQ ID NO:14.
AAY90818 standard; protein; 119 AA
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                                                                                                                                                                                                                                                                                                                        84US-00577976.
85US-00690750.
86US-00842476.
88US-00190778.
94US-00288981.
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N-PSDB; AAA38902.
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                                                             29-AUG-2000
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21-MAR-1986;
08-MAY-1988;
11-AUG-1994;
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                                AAY90818;
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Length 130; 0; Indels

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New elongase polypeptides which are functional long chain polyunsaturated fatty acid (PURA) elongase polypeptides are described. The elongase catalyses an elongase reaction to produce PURA (24 carbon fatty acid with at least 4 double bonds) such as di-homo-gamma-linoleic acid (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14), elocosapentanoic acid (20:5Delta8,11,14), docosatetraenoic acid (22:5Delta3,16,19), docosatetraenoic acid (22:5Delta4,7,10,13,16,19), bURA produced is useful in foodsutifs, dietary supplements and in pharmaceutical compositions which can then be used to elavate PURA levels of an animal or plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide comprising functional long chain polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used to produce PUFA for foodstuff, dietary supplement or pharmaceutical
                                                Elongase; polyunsaturated fatty acid; PUFA; dietary supplement; pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid; arachidonic acid; elcosapentanoic acid; docosatrienoic acid; docosatetraenoic acid; docosatetraenoic acid; docosapentaenoic acid; docosabentaenoic acid;
              Human sequence (BAC207d4) related to PUFA elongase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 10, 42pp, English.
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2000GB-00003869
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18-FEB-2000;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q8ncd1 homo sapien	Q8tep9 homo sapien	Q8ymi3 anabaena sp	Q9h5j4 homo sapien	Q92016 rattus norv	Q8ce45 mus musculu	Q92015 mus musculu	Q9xx32 caenorhabdi	Q93iz9 streptomyce	Q9btv4 homo sapien	Q8nc30 homo sapien	Q96f19 homo sapien	Q9h076 homo sapien	Q9dbs1 mus musculu	Q8pkv6 xanthomonas	Q8ebw6 shewanella
Ð	Q8NCD1	Q8TEP9	Q8YMI3	Q9H5J4	Q920L6	Q8CE45	Q920L5	Q9XX32	Q931Z9	Q9BTV4	Q8NC30	Q96F19	Q9H076	Q9DBS1	Q8PKV6	QBEBW6
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% Query Match Length DB	240	255	263	265	267	267	267	338	371	400	400	400	400	400	403	418
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**NEDLINE=21595285; PubMed=11759840; Ruritz T., Sasamoto S., MEDLINE=21595285; PubMed=11759840; Ruritz T., Sasamoto S., A. Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., A. Kaneko T., Nakamura M., Ishikawa A., Kawashima K., Kimura T., Kinda Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., A. Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Yasuda M., Yasuda S., Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Yasuda M., Yasuda M., Yasuda M., Yamada M., Yasuda M., Yasuda M., Yasuda M., Yasuda M., Habaena Sp. Strain PCC 7120."; Ling R. Baris, Appolasses, Baris General S., Sugimoto S., Sugimoto M., Pirothetical protein; Complete proteome.

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     TIŜSUE=Spleen;
Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
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Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
NCB1_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spleen."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. NOM TEP 1
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SEQUENCE 255 AA; 28454 MW; BF85941BB2012999 CRC64;
                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLO0144 protein (Fragment)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein All4950.
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108 YM
11 ON 11 M
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13 ON 14 M
14 ON 14 M
15 ON 16 M
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PRELIMINARY;

Q9H5J4 Q9H5J4;

RESULT 4 Q9H5J4

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                                                                                                                                                                                                                                                                  Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., "NED human cDNA sequencing project."; submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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EMBL; ABO71986; BAB669881.; -. GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR020276; GNSI_SUR4.
InterPro; IPR020276; GNSI_SUR4.
PROSITE; PF01151; ELO; 1.
SEQUENCE 267 AA; 31624 MW; 4026C9CB33ED0743 CRC64;
                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Otordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Inagaki K., Aki T., Fukuda Y., Kawamoto S., Shigeta S., Ono K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 11; Length 267; 100.0%; Pred. No. 68; 0; Indels (ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 4; Length 265; 100.0%; Pred. No. 67; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO27031; BAB15632.1; -.
EMBL; BC001305; AAH01305.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:15829; ELOVLG.
GO:0014021; C:integral to membrane; IEA.
InterPro; IPR002076; GNS1_SUR4.
PFam; PF01151; ELO; 1.
PROSTITE; PS01188; ELO; 1.
HYDOCHELICAL protein.
SEQUENCE 265 AA; 31376 MW; 01234E0EEF6CE341 CRC64;
01.MAR-2001 (TrEMBLrel. 16, Created)
LUMR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ23378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                            (Human)
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSUE=Placenta;
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RESULT 8
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STRAIN-C57BL/6J; TISSUE-Skin;
STRAIN-C57BL/6J; TISSUE-Skin;
STRAIN-C57BL/6J; TISSUE-Skin;
The STRAIN-C57BL/6J; TISSUE-Skin;
The STRAIN-C57BL/6J; TISSUE-Skin;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acyl elongase (Long-chain fatty-acyl elongase) (Myelination associated SUR4-like protein).
BLOVLG OR FAE OR LCE OR MASR.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mummalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=21576178; PubMed=11567032;
Moon Y.A., Shah N.A., Mohapatra S., Warrington J.A., Horton J.D.;
Identification of a Mammalian Long Chain Fatty Acyl Elongase
Regulated by Sterol Regulatory Element-binding Proteins.";
J. Biol. Chem. 276:45358-45366 (2001).
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TATAIN-CS7816, TISSUB-Liver;

Matsuzaka T., Shimano H.;

"murine complete cds for new fatty acyl elongase similar to cig30
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Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01151; BLO; 1. SEQUENCE 267 AA; 31601 MW; 4031F9C503E4DD23 CRC64;
                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Long chain fatty acyl elongase.
ELOVIA OR LCE.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 AA.
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170 NYGVH 174
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SEQUENCE FROM N.A.
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                                                                                                                      RESULT 6
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Strausberg R.;
Submitted (A.P. 2013) to the EMBL/GenBank/DDBJ databases.

EMBL, AB072039; BAB6844.1; -

EMBL, A8052453; AAL14239.1; -

EMBL, A8053453; AAL14239.1; -

EMBL, A80560, AAM13450.1; -

EMBL, BC051041; AAH51041.1; -

MOD, MGI.2186528; Elovid.

GO; GO:0010747; F:transferase activity, transferring groups o. .; IDA.

GO; GO:0030497; P:transferase activity, transferring groups o. .; IDA.

GO; GO:0030497; P:transferase activity, IDA.

InterPro; IPR002076; GNS1_SUR4.

FEAM; PR01151; ELO; 1.

PROSITE; PS011189; ELO; 1.

SEQUENCE 267 AA; 31610 MW; 4026C9CB33FDDD23 CRC64;
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"Genome sequence of the nematode C.elegans: A platform for investigating biology.";

"Investigating biology.";

"Interpro; Inprodess; Information of transcription, DNA-dependent; IEA.

"Interpro; Inprodess; Information information."

"Interpro; Inprodess; Information."

"Interpro; Informatio
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
Nagarajan R., Le N.H., Mahoney H., Araki T., Milbrandt J.D., "Deciphering Peripheral Nerve Myelination Using Schwann Cell Expression Profiling.", Expression Profiling.", but EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 11; Length 267; 100.0%; Pred. No. 68;
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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STRAIN-CZECH II; TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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MEDLINE=99069613; PubMed=9851916;
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nes 5; Conservative
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Best Local Similarity 100. Matches 5; Conservative
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SEQUENCE FROM N.A.
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                                           FISSUE=Brain;
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Q8NC30;
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Q96F19
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ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOL1; 1.
SMART; SM00399; ZnF_C4; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 338 AA; 39146 MM; 76526E469D05868A CRC64;
                                                                                                                                                                                                           Gaps
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MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Göble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandraam M.A., Rutherford K., Ruther S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Complete genome sequence of the model actinomycete Streptomyces
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ14971 (Hypothetical protein FLJ14851).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 16; Length 371; 100.0%; Pred. No. 98; 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
Bacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1902,
                                                                                                                                                           Query Match
100.0%; Score 31; DB 5; Length 338;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels
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SEQUENCE 371 AA; 39201 MW; 5A54095CBFCD8C27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative secreted peptidase.
SCO7521 OR SCBAC25F8.13C.
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Nature 417:141-147(2002).
EMBL; A1939131; CAC42148.1; -.
HSSP; P15555; ICEF.
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Best Local Similarity 100...
5, Conservative
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                                                                                                                                                                                                                                                                                 26 NYGVH 30
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AC 098TV
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DT 01-JU
DT 01-JU
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BMBL, AKOT5010; BACI1350.1; --
Hypothetical protein.

SEQUENCE 400 AA, 44859 MW, 14F5401ADF9C32A6 CRC64;
                                                                                                         DEPUBLIES FROM M. And Placenta;

SEGUENCE TY, Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Ranase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Makamatua A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR027037; BAB55348.1; -..

EMBL; AR027757; BAB55348.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypotherical protein.
SEQUENCE 400 AA, 44875 MW, 70FDDD4ED1AA11DF CRC64;
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01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ90529.
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Best Local Similarity lvv...
5, Conservative
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01-OCT-2002
01-OCT-2002
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STRAIN=C57BL/6J; TISSUE=Lung;
STRAIN=C57BL/6J; TISSUE=Lung;
MadDINRE-21885660; PubMed=112178E1;
Makawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, AL136916; CAB66850.1; -.
Hypothetical protein.
SEQUENCE 400 AA, 44831 MW, BD998B0BB73120B4 CRC64;
                                                                                                                              100.0%; Score 31; DB 4; Length 400; llarity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0; Indels
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                                                 TISSUE-Oterus,
Straubberg R.;
Straubberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011719, AAH11719.1; -.
Hypothetical protein.
SEQUENCE 400 AA; 44847 MW; BD89DB4BB7313GF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DBS1;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1200015A22Rik protein (RIKEN cDNA 1200015A22 gene).
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Last annotation update)
                                                                                                                                                                                                                                                   400 AA.
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01-MAR-2001 (TrEMBLrel. 16
01-OCT-2002 (TrEMBLrel. 27
Hypochetical protein.
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Best Local Similarity 100.
Matches 5; Conservative
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nes 5; Conserv
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                                          SEQUENCE FROM N.A.
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                    NCBI_TaxID=9606;
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Matches
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE 5. ATCC 13902 / XV 101;

MEDLINE=2202145; PubMed=12024217;

A SIVA A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;

A Ga Silva A.C.R.; Machael C.B.; Van Sluys M.A.; Almeida N.F.;

A Alves L.M.C.; do Amaral A.M.; Bartolini M.C.; Camargo L.B.A.;

Camarotte G.; Cannavan F.; Cardozo J.; Chambergo F.C.; Capina L.P.;

A Tital J.B.; Ferrelar A.J.S.; Ferrelar R.C.C.; Ferro M.I.T.;

Ratsuyama A.M.; Kishi L.T.; Leite R.P.; Lemos B.G.M.; Lemos M.V.F.;

A Ratsuyama A.M.; Kishi L.T.; Leite R.P.; Lemos E.G.M.; Lemos M.V.F.;

A Martins E.C.; Machado M.A.; Madaira A.M.B.N.; Martinez-Rossi N.M.;

Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;

Perform H.A.; Rossi A.; Sana J.A.D.; Silva C.; de Souza R.F.;

A Spinola L.M.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.;

Trindade dos Santos M.; Truffi D., Tsai S.M.; White F.F.;

Sctubal J.C.; Kitajima J.P.;

Trindade dos Santos M.; Truffi D., Tsai S.M.; White F.F.;

Comparison of the genomes of two Xanthomonas pathogens with differing Nature 417; 459-463 [2202].
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Fuels S., Matsuo Y., Nikaido I., Peoole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinnich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamioto N., Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshima Borita A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
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Bacteria; Forebacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
WCBI_TaxID=92829;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX004778; BAB23556.1; -.
EMBL; AX004778; AAH24933.1; -.
MGD; MGI:921372; 1200015A22Rik.
SEQUENCE 400 AA; 44783 MW; SA9732B4214D4316 CRC64;
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR006076; Fad_oxred.
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DR Pfam; PF01266; DAO; 1.

KW Complete proteome.

SQ SEQUENCE 403 Aa; 44543 MW; A8394D0E38880EEF CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 16; Length 403;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps. 0;

Qy 1 NVGVH 5

Db 163 NVGVH 167

Search completed: October 6, 2004, 16:33:42

Job time: 22.7544 secs
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WEDLINE=86108364; PubMed=3943519;
WARDLINE=86108364; PubMed=3943519;
Hoejrup P., Andersen S.O., Roepstorff P.;
Hoejrup P., Andersen S.O., Roepstorff P.;
Tisolation, characterization, and N-terminal sequence studies of
Tisolation, characterization, and N-terminal
Tisolation, characterization, and N-terminal
Eur. J. Blochem. 154:153-159(1986).

"Eur. J. Blochem. 154:153-159(1986).

"I FUNCTION: Component of the cuticle of migratory locust which
contains more than 100 different structural proteins.

"I FUNCTION: Component in many proteins constituting the
protective envelope of other species.

"I FIREARY: Contains I cuticle consensus domain.

PIR. 505638; S05638.

"InterPro: IPR000618; Insect cuticle.

"REPROSED TOWNICHED."

"PRINTS: PR00379; Cutitin bind 4; 1.
                        staphylococ
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pleuronecte
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01-CCT-1989 (Rel. 12, Last sequence update)
01-CCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cuticle protein 8 (LM-8) (LM-ACP 8).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
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            Q9ez11
Q8nws4
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Pred. No. 5.5;
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                                                                                   Search time 3.07018 Seconds (without alignments) 84.800 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pets6-his3-dedl gene region.";
Nucletc Acids Res. 13:8587-8661(1985).
Nucletc Acids Res. 13:8587-8661(1985).
PUNCTION: Encodes an essential ribose methyltransferase that specifically modifies to 2'-O-methylguanosine a universally conserved nucleotide, G-2270, in the peptidyl transferase center of the mitochondrial large ribosomal RNA (218). This modification seems to be important for the normal accumulation of this latter
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EMBL; X0345; CAA27002.1; -.

EMBL; X3881; CAA27002.1; -.

EMBL; X58881; CAA27002.1; -.

Germonline; 143789; -.

SGD; S000573; PETS6.

GO; GO:0005739; C:mitcochondrion; IDA.

GO; GO:000154; P:RNA medification; IDA.

InterPro; IPR00441; rRNA_medification; IDA.

InterPro; IPR004431; rRNA_methyl_3.

InterPro; IPR0048431; SpoU_methylase.

Pfam; PF00588; SpoU_methylase.
                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ribose methyltransferase PET56 (EC 2.1.1.-) (Mitochondrial large ribosomal RNA ribose methylase) (218 rRNA [GM2251] 2'0-
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sirum-Connolly K., Mason T.L.; "Functional requirement of a site-specific ribose methylation in
                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and transcriptional mapping of the yeast
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Pred. No. 15;
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SEQUENCE FROM N.A.
Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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TIGRAMS, TIGR00186; rRNA methyl 3; 1.
Mitochodrion, Transferaes; Methylransferaee.
SEQUENCE 412 AA; 46387 MW; C01B10254C0EDEA8 CRC64;
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-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: TO S. POMBE SPEC1347.13C.
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94090319; PubMed=8266080;
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01-FEB-1996 (Rel. 33, Last seq
30-MAY-2000 (Rel. 39, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                             Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myomesin 2 (M-protein) (165 kDa titin-associated protein) (165 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRANT=Bristol N2;
Du Z., Gatung S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 1; Length 435; 100.0%; Pred. No. 16; 0; Indels cive 0; Mismatches 0; Indels
                                              01.FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 51.5 kDa protein D2024.3 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51480 MW; F7940A74A1969914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-Skeletal muscle;
MEDLINE=94095665; Pubmed=7505783;
Vinkemeler U., Obermann W., Weber K., Fuerst D.O.;
  435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PFULLD1; ALV., 1.
PROSITE; PSO1188; ELO.; 1.
Hypothetical protein; Transmembrane.
62 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; D2024.3; CE04292.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          connectin-associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U41011; AAA82288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5, Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, T34200; T34200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 NYGVH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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5; Conservative

Matches

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Gaps

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0; Indels

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Brevibacillus parabrevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
17yrocidine syntherase III [Includes: ATP-dependent asparagine
adenylase (AsnA) (Glutanine activase); ATP-dependent tyrosine
adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase
(ValA) (Valine activase); ATP-dependent crnithine adenylase (Ornithline activase);
(Ornithline activase); ATP-dependent leucine adenylase (Leucine
TYCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
"The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron microscopy of two titin-associated proteins.",

J. Cell Sci. 106:319-330 (1993).

-!- FUNCTION: Major component of the vertebrate myofibrillar M band.
Blinds myosin, titin, and light meromyosin. This binding is dose
                                                                                                                                                                                                                                                                                                                                  I.e protein; Thick filament; Repeat.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 1.
FISHONECTIN TYPE-III 1.
FISHONECTIN TYPE-III 2.
FISHONECTIN TYPE-III 3.
FISHONECTIN TYPE-III 4.
FISHONECTIN TYPE-III 4.
FISHONECTIN TYPE-III 5.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
                                                                -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 1465; Pred. No. 51; 0; Mismatches 0; Indels C
                                                                                                                                                                           PRT; 6486 AA.
                                                                                                                                                                                                                                                                               MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                   EMBL; X69089; CAA48832.1; -. PIR; S43529; S43529.
                                                                                                                                                                                                                                                                                                                                                                                                                                         164793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 469
                                                                                                                                                                                                                                                                                                                                                                                                                       1211
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 NYGVH 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                         1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYCC_BR
030409;
                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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BREPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANGOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLIC DECAPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-ORN-LEU), B, C, AND D, IN WHICH PHE, AT POSTTIONS 3, 4, AND TYR RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE
                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 8185 / IAM 1031 / IFO 3331 / NCDO 717 / NCIB 8598;
STRAIN=ATCC 8185 / PubMed=9352938;
MOCIZ H.D., Marahiel M.A.;
"The tyrocidine biosynthesis operon of Bacillus brevis: complete nucleotide sequence and biochemical characterization of functional
                                                                                                                                                                                                                                                                                   internal adenylation domains.";
J. Bacteriol. 179:6843-6850(1997).
-!- FUNCTION: INCORPORATES SIX AMINO ACIDS (FOR TYROCIDINE A, ASN, GLN, TYR, VAL, ORN, AND LEU) IN THEIR L-CONFIGURATION INTO THE PEPTIDE PRODUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis.
-1- SUBUNIT: LARGE MULTIENZYME COMPLEX OF TYCA, TYCB AND TYCC.
-1- DOMAIN: CONSISTS OF SIX MODULES, AND HARBORS A PUTATIVE
THIORSTERAGE DOMAIN AT ITS C-TERMINAL END. EACH MODULE
INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN B
FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE
ADENYLATION THIOLATION, CONDENSATION (NOT FOR THE INITIATION
MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION
(OPTIONAL).
Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contains 6 covalently bound phosphopantetheines (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN 1 (ASPARAGINE-ACTIVATING).
DOMAIN 2 (GLUTAMINE-ACTIVATING).
DOMAIN 3 (TYROSINE-ACTIVATING).
DOMAIN 4 (VALINE-ACTIVATING).
DOMAIN 5 (ORNITHINE-ACTIVATING).
DOMAIN 6 (LEUCINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 4.
ACYL CARRIER (ACP) 4.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 6.
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PROSTIE; PRO012; PHOSPHOPANTETHEINE; 6.
PROSTIE; PSO045; AMP BINDING; 6.
PROSTIE; PSSO075; ACP DOWAIN; 6.
Ligase, Antibiotic biosynthesis; Phosphopantetheine;
Multifunctional enzyme; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 6 acyl carrier domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF004835, AAC45930.1; -. PDS, 1DNY; 17-MAY-00.
InterPro; IPR000873; AMP-bind.
InterPro; IPR001843; AMP-bind.
InterPro; IPR001842; Condensatn.
InterPro; IPR001842; Ppaintne S.
InterPro; IPR001879; Ser_estrs.
InterPro; IPR001879; Ser_estrs.
InterPro; IPR001871; Thioesterase.
Pfam; PF00580; Condensation; 6.
Pfam; PF00580; Condensation; 6.
Pfam; PF00580; Thioesterase; 1.
                              NCBI_TaxID=54914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: Co
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25536
35996
56596
2007
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51124
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REPEAT
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DOMAIN
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RESULT 7
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Similarity).

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                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=56601 / Serggroup Icterohaemorrhagiae / Serovar lai;

MEDLINB=22588143; PubMed=1212204;

Ren S.-X., Fu G., Jaing M.-G., Zeng R., Miao Y.-G., Xu H.,

A chang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-G., Ja J., Tu Y.-F.,

A chang Y.-X., Zhu G.-F., Wan M., Huang H.-L., Sheng H.-H., Yin H.-F.,

A chang Y.-X., Shen Y., Qiang B.-G., Kai Q.-C., Wang S.-Y., Ma W.,

A co Z.-J., Shen Y., Qiang B.-G., Xia Q.-C., Guo X.-K., Danchin A.,

A configurations I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

A unique physiological and pathogenic features of Leptospira

Interrogans revealed by whole-genome sequencing.";

Nature 422:888-893(2003):

C. CARALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

Phosphate + glutamate + carbamoyl phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                Leptospira interrogans.
Bacteria, Spirochaetes, Spirochaetales, Leptospiraceae, Leptospira
                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                         ;
                                                                                                Length 6486;
                                                                                                                       0; Indels
                                                                         CRC64;
                                                                         4934900AF07DF786
                                                                                                Score 31; DB 1; I Pred. No. 2.2e+02;
                                  PHOS PHOPANTETHEINE
PHOS PHOPANTETHEINE
PHOS PHOPANTETHEINE
   PHOSPHOPANTETHEINE
               PHOSPHOPANTETHEINE PHOSPHOPANTETHEINE
                                                                                                                                                                                                                                    363 AA
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAÞ; MF_01209; -; 1.
InterPro; IPR066274; CarA synth smal
InterPro; IPR001317; CP_synthGATase.
InterPro; IPR002474; CP_synthSmall.
InterPro; IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00988; CPSase sm chain; 1.
Pfam; PF00117; GATase; 1.
                                                                         724011 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE011305; AAN48438.1; -.
                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                    STANDARD;
               2037
                                     4110
5154
6197
                                                                          AA;
                                                                                                                                                                       2664 NYGVH 2668
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                1 NYGVH 5
                2037
3075
4110
5154
6197
6486
                                                                                                                                                                                                                                                                                                                       CARA OR LA1239.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=173;
                                                                                                                                                                                                           RESULT 6
CARA_LEPIN
ID CARA_LEPIN
AC Q8F6R2;
                                                             BINDING
               BINDING
BINDING
BINDING
   BINDING
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RAKELINE-S90444033, PubNed=2984377;

Runst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barenscher L., Brans A., Braun M., Brignell S.C., Bron S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Rh Brouillet S., Bourschi C.V., Connerton I.F., Cummings N.J., Daniel R.A., Britz C., Eron S., Emerson P.T., Rh Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Pujita W., Fujita Y., Fuma S., Galizzi A., Galleron N., Rh Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Aringeppi G., Guy B.J., Haga K., Halcoh J., Harvood C.R., Henaut A., Guiseppi G., Guy B.J., Haga K., Halcoh J., Harvood C.R., Henaut A., Guiseppi G., Guy B.J., Haga K., Halcoh J., Harvood C.R., Henaut A., Goris B., Karamata D., Kasahara Y., Rlein C., Karamata D., Kasahara Y., Rlein C., Lazarevic V., Koetter P., Koningstein G., Krogh S., Kumano M., Acobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Mediau R., Levine A., Liu H., Masuda S., Mauel C., Lazarevic V., R. Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M., Rapor U., Pohl T.M., Portecelle D., Porwollik S., Prescott A.M., Anone D., O'Reilly M., Potterelle D., Porwollik S., Prescott A.M., Raconi B., Schoetch B., Rapoport G., Rey M., Reynolds S., Sato T., Scanlan E., Roche B., Roscifone F., Schoetch M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K., Atari A., Manbutt R., Wedler E., W
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MEDLINE=21242727; PubMed=11344136;
Schultz A.C., Nygaard P., Saxild H.H.;
"Functional analysis of 14 genes that constitute the purine catabolic pathway in Bacillus subtilis and evidence for a novel regulon controlled by the PucR transcription activator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                          Similarity 80.0%; Pred. No. 22; 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                            GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
TIGRFAMS; TIGRO1368; CPSaseIIsmall; 1.
PROSITE; PSO0442; GATABETYPE; 1; 1.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase; Complete proteome.
                                                                                                                                                                                            174 363 GLUTAMINE AMIDOTRANSFERASE
253 253 GATASE (BY SIMILARITY).
363 AA; 40261 MW; 58BD2BB8F43D0BEE CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uric acid permease pucJ. PUCJ OR BSU32430.
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Best Local Similarity
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ID FUCJ_BACSU
AC 032139;
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96.8%;
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    J. Bacteriol. 183:3293-3302(2001).
    I-FUNCTION: Upptake of uric acid.
    SUBCELLULAR LOCATION: Integral membrane protein (Probable).
    INDUCTION: Expression is very low in excess nitrogen (glutamate plus ammonia) and is nduced during limiting-nitrogen conditions (glutamate). Expression is further induced when allantoin or uric acid are added during limiting-nitrogen conditions.
    SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.

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01-FED-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable alpha-amylase C23D3.14c precursor (EC 3.2.1.1) (1,4-alpha-D-SPAC23D3.14c).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE=21848401; PubMed=11859360;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Barbam D., Bowann S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
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9B97CCC42330C087 CRC64;
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 1;
Pred. No. 27;
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POTENTIAL.
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TIGRPAMS, TIGRO0801, nce2; 1.
SS01116, XANTH URACIL PERMASE,
Transmembrane; Transport; Complete proce
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POTENTIAL.
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InterPro, IPR006042, Xan ur permease.
InterPro, IPR006043, XanE/urac/vitC.
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449 AA;
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TRANSMEM 11
TRANSMEM 41
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Q09840;
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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mangall K., Murphy L., Nibbett D., Odell C.,
RA Goliver K., C'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Gabel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Goffeau A., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimena Z., Sumstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
R. The genome sequence of Schizosaccharomyces pombe.",
R. Maure 41:8191-880(2002)
C. -- CARLYTIC ACTIVITY: Endohydrolysis of 1,4-lpha-glucosidic
Linkages in oligosaccharides and polysaccharides.
C. -- CARLYTIC ACTIVITY: Belongs to family 13 of glycosyl hydrolases.
C. -- CIRLARITY: Belongs to family 13 of glycosyl hydrolases.
C. -- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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PIR; T38299; S62505.
HSSP; P10229; TAAA.
GeneDB SPORMe; SPAC23D3.14c; -.
InterPro; IPR006589; Alp amyl cat_sub.
InterPro; IPR00647; Alpha_amyl_cat.
Ffam; PF00128; alpha_amylase; 1.
SMART; SM00642; Aamy; Laxbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; Glycoprotein.
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BY SIMILARITY
BY SIMILARITY.
CALCIUM 1 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
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CALCIUM 2 (BY SIMILARITY).
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .)
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Pred. No. 35;
1; Mismatches 0; Indels
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64 BY
191 BY
311 BY
291 N-
332 N-
67004 MW;
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373
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680 AA;
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CARBOHYD
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CARBOHYD
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MEDLINE=92005720, PubMed=1913827,
Legouis R., Hardelin J.-P., Levilliers J., Claverie J.-M., Compain S.,
Wunderle V., Millasseau P., 1e Pasalier D., Cohen D., Caterina D.,
Bougueleret L., Delemarre-Van de Waal H., Lutfalla G., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                              "Structure of the X-linked Kallmann syndrome gene and its homologous pseudogene on the Y chromosome."; Nat. Genet. 2:305-310(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-71 FROM N.A.
MEDLINE=96069588; PubMed=7590336;
Cohen-Salmon M., Tronche F., del Castillo I., Petit C.;
"Characterization of the promoter of the human KAL gene, responsible for the X-chromosome-linked Kallmann syndrome.";
Gene 164:235-242(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Initial characterization of anosmin-1, a putative extracellular matrix protein synthesized by definite neuronal cell populations in the central nervous system."; U. Cell Sci. 109:1749-1757(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardelin J.-P., Levilliers J., Blanchard S., Carel J.-C.,
Leutenegger M., Pinard-Bertelletto J.-P., Bouloux P., Petit C.,
"Heterogeneity in the mutations responsible for X chromosome-linked
                                                                                                                                                                                                                                                                                                                                                                                        [3] SEQUENCE FROM N.A. MSDLINE=92018217; PubMed=1922361; Franco B., Guioli S., Pragliola A., Inceri B., Bardoni B., Franco B., Guioli S., Maetrini E., Pieretti M., Taillon-Miller P., Brown C.J., Willard H.F., Lawrence C., Persico N.G., Camerino G., Ballabio A., Agene deleted in Kallmann's syndrome shares homology with neural adhesion and axonal path-finding molecules."; Nature 353:529-536(1991).
                                                        01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Anosmin 1 precursor (Kallmann syndrome protein) (Adhesion molecule-
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               "The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules."; cell 67:423-435(1991).
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MEDLINE=56429296; PubMed=8832397;
Soussi-Yanicostas N., Hardelin J.-P., del Mar Arroyo-Jimenez M.,
Ardouin O., Legouis R., Levilliers J., Traincard F., Betton J.-M.
Cabanie L., Petit C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VALIANT KALI LYS-514, AND VARIANT VAL-534.
MEDINDE-98251583; PubMed-9589672;
Maya-Nunez G., Zenteno J.C., Ulloa-Aguirre A., Kofman-Alfaro S.,
Mendez J.E.;
"A recurrent missense mutation in the KAL gene in patients with
                                                                                                                                                                                                                                                                                          [2]
REVISIONS.
MEDLINE-99265164; PubMed=1303284;
del Caștillo I., Cohen-Salmon M., Blanchard S., Lutfalla G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [6]
VARIANT KALI LYS-267, AND VARIANT VAL-534.
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                                                                                               like x-linked).
Karı OR Kar OR ADMLX OR KALIGI.
                                              01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last seq
10-OCT-2003 (Rel. 42, Last anno
                        STANDARD;
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                        KALM HUMAN P23352;
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R. J. Tithed Kallmann's syndrome, "y.

1. Tith. Endocrinol, Weath. 89:1650-1650(1999).

1. FUNCTION: May be an addesion-like molecule with anti-protease control and the control of the co
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SEQUENCE 70 Nubmed=9169871;

MEDLINE=97313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

MEDLINE=974061261 D., Hillbert M., Helling U., Heunann K.,

Heuss-Neitzel D., Hilbert H., Hillger F., Kleine K., Koetter P.,

Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Meller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Meller-Auer S., Nentwich B., Scholler P., Schwager C., Schwarz S.,

Noterelle D., Purnelle B., Rechmann F., Schwager C., Schwarz S.,

Noterelle D., Purnelle B., Rechmann P., Schwager C., Schwarz S.,

Noterendeels P., Voet M., Volckaert G., Voes H., Wambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=F113; MEDLINE=92237270; PubMed=1570306; Januebusch A.G., Klausner R.D., Dancis A., Foman D.G., Anderson G.J., Hinnebusch A.G., Klausner R.D., "Ferric reductase of Saccharomyces cerevisiae: molecular characterization, role in iron uptake, and transcriptional control by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jinorg. Biochem, 47:249-255(1992).

-!- FUNCTION: Reductase activity that acts on ferric iron chelates external to the cell. Plays a role in iron uptake. May participate in the transport of electrons from cytoplasm to an extracellular substrate (ferric ion) via FAD and heme intermediates. May also participate in Cu(II) reduction and Cu(I)
                                           Gaps
                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Ferric iron reduction and iron assimilation in Saccharomyces cerevisiae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CĀTALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).
-!- COFACTOR: FAD (Frobable).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: BY IRON DEPRIVATION. REPRESSED BY IRON UPTAKE.
-!- SIMILARITY: Belongs to the FRE / CYBB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE=93067491; PubMed=1431884;
Anderson G.J., Lesuisse E., Dancis A., Roman D.G., Labbe P.,
Klausner R.D.;
            DB 1; Length 680; 41;
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 89:3869-3873(1992).
                                                                                                                                                                          686 AA.
                                        Mismatches
            Score 30;
Pred. No.
                                                                                                                                                                          PRT;
          96.8%;
                                        Conservative
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 387:87-90(1997).
          Query Match
Best Local Similarity
                                                                                       224 NYGIH 228
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                    'n
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                    1 NYGVH
                                        4,
                                                                                                                                                                          FRE1 YEAST
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FRE1_YEAST
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                               FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
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2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
N-LINKED (GLCNAC. . . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                             GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:000593; F:ferric-chelate reductase activity; IDA.
GO; GO:0015677; P:copper ion import; IDA.
GO; GO:0006826; P:iron ion transport; IDA.
InterPro; IPR002916; Ferric reduct.
InterPro; IPR01994; Ferric reduct.
Oxidoreductase; Electron transport; Transmembrane; Iron transport;
FAD; NAD; Copper; Glycoprotein; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 18:553-560(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 1; Length 686; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7F6BB3B93A95D6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG Hil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAD (POTENTIAL).
NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=79124695; PubMed=420800;
                                                                   EMBL; M86908; AAA34608.1; --
EMBL; U14913; AAB6724.1; --
PIK; S30075; S30075;
Germonline; 142276; --
SGD; S0004204; FRE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78853 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             686 AA;
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|135 NYGIH 139
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P01771;
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CARBOHYD
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NP_BIND
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CARBOHYD
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SEQUENCE
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? 212
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                                                                                                                                                                                                                                                                                                                                                212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
MADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD).
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hough R.F., Lingam A.T., Bass B.L.; "Caenorhabditis elegans mRNAs that encode a protein similar to ADARs derive from an operon containing six genes."; Nuclaic Acids Res. 27:344-3432(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I - FUNCTION: May donate electrons to ubiquinone.
-I - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-I - CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-I - COFACTOR: Binds 2 4Fe-4S clusters per subunit (By similarity).
-I - SUBUNIT: Complex I is composed of 45 different subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- SIMILARITY: Belongs to the complex I 23 kDa subunit family.
-!- SIMILARITY: The iron-sulfur centers are similar to those of
                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                 Length 121;
                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                    121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
GO; GO:0006955; P:immune response; NAS.
Interbro; IPR007110; Ig-like.
Interbro; IPR00356; Ig-v.
Pfam; PF00047; ig: 1.
SMART; SM00406; IGv.
ISMART; SR00406; IGv.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                 Score 28; DB 1;
Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSF; P00198; 2FDN.
Wormbep; 720445; CE00832.
InterPro; IPR001450; 4Fe4S_ferredoxin.
Pfam; PP00037; fer4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterial-type 4Fe-4S ferredoxins.
                                                                                                                                                                             IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
MEDLINE-99377169; PubMed=10446229;
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                                                                                                                                                                                                                                                                                                      90.3%;
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PIR; T16914; T16914.
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 NYGMH 35
                                                                                                                                                                                                                                                                                                                                                                                                     1 NYGVH 5
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SEQUENCE
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Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Satto K., Nishikawa T., Kimura K.,
Yamashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                   113 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
116 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
123 IRON-SULEUR 2 (4FE-4S) (BY SIMILARITY).
154 IRON-SULEUR 2 (4FE-4S) (BY SIMILARITY).
155 IRON-SULEUR 2 (4FE-4S) (BY SIMILARITY).
158 IRON-SULEUR 2 (4FE-4S) (BY SIMILARITY).
162 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
163 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
164 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
167 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
168 IRON-SULEUR 1 (4FE-4S) (BY SIMILARITY).
                                                                                                                                                       23 KDA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
Oxidoreductase; NAD; Ubīquinone; Mitochondrion; Transit peptide;
Iron-sulfur; 4Fe-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDF6_HUMAN STANDARD; PRT; 337 AA.
096NR6; Q9H346;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neurogenic differentiation factor 6 (NeuroD6) (My051 protein)
                                                                                                           MITOCHONDRION (BY SIMILARITY).
NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 1; Length 212;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 37;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity 80.0%;
4; Conservative
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or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: Specific to the nervous system of both embryos and adults. Highest levels in the cortical plate of the cerebrum.
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Neurogenic differentiation factor 6 (NeuroD6) (Atonal protein homolog
2) (Helix-loop-helix protein mATH-2) (MATH2) (NEX-1 protein).
NEUROD6 OR ATOH2 OR ATH2 OR NEXI.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/J;
MEDLINE=955673; PubMed=7744035;
Shimizu C., Akazawa C., Nakanishi S., Kageyama R.;
"MATH-2, a mammalian helix-loop-helix factor structurally related to
the product of Drosophila proneural gene atonal, is specifically
Expressed in the nervous system.";
Eur. J. Blochem. 229:239-248(1995).
                                                                                               Transcription regulation; Activator; DNA-binding; Nuclear protein.

DOMAIN 54 63 POLY-GLU.

DOMAIN 80 86 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                ô
                                                                                                                                                                          Score 28; DB 1; Length 337;
Pred. No. 58;
1; Mismatches 0; Indels
                                                                                                                              BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF.
6B0F4127AC0F809E CRC64;
or send an email to license@isb-sib.ch)
                    EMBL; AF063609; AAG43167.1; ALT_FRAME.
EMBL; AK055238; BAB70885.1; -.
                               EMBL, AK055238, BAB70885.1; -.. Genew; HGNC:13804; NEDROD6.
InterPror, IPRO01092; HLH_basic.
Pfam, PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
                                                                                                                                                    38705 MW;
                                                                                                                                                                          90.3%;
                                                                                                                                                              Query Match
Query Match
Best Local Similarity 80.vv.,
Best hes 4; Conservative
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                                                                                                                                                       337 AA;
                                                                                                                                                                                                                                           286 NYGMH 290
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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NDF6_MOUSE
ID _NDF6_MOUSE
                                                                                                                     DOMAIN
DNA BIND
                                                                                                                                                    SEQUENCE
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Gaps
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DOMAIN

S4 63 POLY-GLU.

DOMAIN

S0 86 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)

DAMAIN

BASIC DOMAIN

DOMAIN

107 147 HELIX-LOOP-HELIX MOTIF.

SEQUENCE 337 AA; 38644 MW; 35C18ACD8EEIEFBA CRC64;
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MEDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region
from 84.5 to 86.5 minutes";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlosser A., Meldorf M., Stumpe S., Bakker B.P., Epstein W.; "TrkH and its homolog, TrkG, determine the specificity and kinetics of cation transport by the Trk system of Escherichia coli."; J. Bacteriol. 177:1908-1910(1995).
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SPECIES=E.coli; STRAIN=K12 / MG1655;

MEDIAR=97426617; bubMd=9278503;

Blattner F.R., Plunkett G. III. Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 337;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRKH ECOLI STANDARD; PRT; 483 AA. P21166; P76769; 01-MAY-1991 (Rel. 18, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Trk system potassium uptake protein trkH. TRKH OR B3849 OR Z5371 OR ECS4777 OR SF3925 OR S3827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
58;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28;
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MEDLINE=91057145; PubMed=2243799;
Nakahigashi K., Inokuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95204366; PubMed=7896723;
EMBL; D44480; BAA07923.1; --
EMBL; U29086; AAC14576.1; --
PIR; 18682; 148682.
PIR; 157038; 157038.
MGD; MGI:106593; Neurod6.
InterPro; IPR001092; HI.H. Dasic.
Fam; PF00010; HI.H; 1.
SMART; SM00353; HI.H; 1.
PROSITE; P550888; HI.H; 1.
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NCBI_TaxID=562, 83334, 623;
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Escherichia caquence between the fada gene and the rrnA operon from Escherichia Cadia Res. 18:6439-643(1990).

Nucleotide Acids Res. 18:6439-643(1990).

Nucleotide Cadia Res. 18:6439-644(12002).

Nucleotide Cadia Res. 18:122(1990).

Nucleotide Cadia Res. 18:122(1990).

Nucleotide Cadia Res. 18:122(1990).

Nucleotide Cadia Res. 18:122(1990).

Nucleotide Cadia Res. 18:12(1990).

Nucleotide Cadia
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Gaps
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                                                      IIGRFAMs; TIGR00933; 2a38; 1.
Transmembrane; Transport; Potassium transport;
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                             -> S (IN REF. 4).
1AA9CC2F83EB509A CRC64;
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V -> IV (IN REF. 4).
C -> S (IN REF. 4).
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Pred. No. 82;
1; Mismatches
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       PIR; G86072; G86072.
EccGene; EG11021; LrkH.
InterPro; IPR003445; Cat_transpt.
InterPro; IPR004772; K_transptTrk.
Pfam; PF02386; TrkH; 1.
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B65190; B65190
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                                                                         Complete proteome.
TRANSMEM 9
TRANSMEM 35
TRANSMEM 70
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us-09-635-974a-2.rpr

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5.1.6	Compugen
version	- 2004
GenCore	(c) 1993
	Copyright

using sw model - protein search, OM protein October 6, 2004, 16:23:59 ; Search time 5.26316 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-2 31 1 NYGVH 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		chain pr	uticle protein	hypothetical prote	cal	protein F56A6.1 [i	cal prot	rRNA (guanosine-2'	cal	g	hist	ical	in,	nthe		hypothetical prote	ermea	hypothefical prote	probable outer mem	probable alpha-amy	adhesion-type prot	Kallmann syndrome	Ö	rob	heavy	Ig heavy chain pre	netical pr	hetical	netical
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ф	Query		00		0	00	•	00	00	00	00	00	00	00	00	00.										-	-				
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Gaps . 0 100.0%; Score 31; DB 2; Length 109; 100.0%; Pred. No. 8.6; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 5; Conservative

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31 NYGVH 35 1 NYGVH 5 $\dot{\delta}$ QQ

A2456

A2456

Johnson Pecursor V region - mouse

Cjspecies: Mus musculus (house mouse)

Cjspecies: Mus musculus (house mouse)

Cjspecies: Mus musculus (house mouse)

Cjspecies: Musculus (house mouse)

Cjspecies: A3456

Rycossion: A3456

Rycommusculus (A5.1 a622, 1989)

A;Title: Variable region primary structures of a high affinity anti-fluorescein immunogla A;Reference number: A32456; MUID:89174706; PMID:2494173

A;Reference: A34466

A;Status: preliminary

A;Residues: preliminary

A;Residues: 1-139 < DOM>
A;Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317

A;Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317

A;Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-116/Domain: immunoglobulin homology <IMM>

Gaps ·. Query Match 100.0%; Score 31; DB 2; Length 139; Best Local Similarity 100.0%; Pred. No. 11; Matches 5; Conservative 0; Mismatches 0; Indels 0; Indels

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A;Residues: 1-325 - MUR>
A;Cross-references: EMBL:AF067217; PIDN:AAC17014.1; GSPDB:GN00019; CESP:F56A6.1
A;Experimental source: strain Bristol N2; clone F56A6
                      Cispecies: Caenorhabditis elegans
Cibate: 29-0c1-1999 #sequence_revision 29-0c1-1999 #text_change 29-0c1-1999
Cibacession: T33082
R;Murray, U.; Rohlfing, T.; O'Neal, D.; Wilson, R.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid F56A6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 325;
protein F56A6.1 - Caenorhabditis elegans (fragment)
                                                                                                                                                                                                        A;Accession: T33082
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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100.0%; Pred. No. 26;
iive 0; Mismatches
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A; Introns: 51/1; 135/3; 202/2; 222/2; 262/1
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Best Local Similarity 100.
Matches 5; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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A;Gene: CESP:F56A6.1
A;Map position: 1
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A,Cross-references:
A,Note: partial CDS
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A,Gene: F56A6.1
A,Map position: 1
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A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. Strain PCC 7120
A,Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. Strain PCC 7120
Giscossion: AF2424
Rikaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analyscession: AF2424
A,Status: preliminary
                                                                                                                                                                                    cuticle protein 8 - migratory locust
Cispecies: Locusta migratoria (migratory locust)
Cjoate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
Cjacession: 805638; B24802
Riklarskov, K.; Hojrup, P.; Andersen, S.O.; Roepstorff, P.
Richen: J. 262, 923-930, 1989
Ajfitle: Plasma-desorption mass spectrometry as an aid in protein sequence determination
A;Reference number: 805638; MUID:90073593; PMID:2590176
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A;Residues: 1-263 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76649.1; PID:g17134088; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics: A;Gene: a114950
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hypothetical protein all4950 [imported] - Nostoc sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-148 < KLA>
R; Hojrup, P.; Andersen, S.O.; Roepstorff, P.
Bur. J Biochem. 154, 153-159, 1986
A; Reference number: A91157; MUID:86108304; PMID:3943519
A; Accession: B24802
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100.0%; Pred. No. 12;
iive 0; Mismatches 0
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A; Residues: 1-53, X', 55-56 < HOJ>
C; Superfamily: migratory locust cuticle protein (C; Reywords: structural protein F:16-19/Region: 4-residue repeat (A-A-P-[AV]) F; 22-25/Region: 4-residue repeat (A-A-P-[AV]) F; 28-31/Region: 4-residue repeat (A-A-P-[AV]) F; 44-47/Region: 4-residue repeat (A-A-P-[AV])
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C;Accession: B87721
Stanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A;RoO() MID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www.sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:chr_I; PIDN:AAC17014.1; PID:g3150502; GSPDB:GN00019; CESP:F56A6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R)Gardner, A.

Submitted to the EMBL Data Library, September 1998
A; Accession: T26588
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-338 < WLL>
A; Residues: 1-338 < WLL>
A; Cross-references: EMBL; AL031632; PIDN: CAA21008.1; GSPDB: GN00023; CESP: Y32B12B.6
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26588
protein F56A6.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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RESULT 5 T33082

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Gaps

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Cispecies: Synechocystis sp.
A; Variety: PCC 6803

E; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C; Accession: 876734

R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N., O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A; M.; Sequence analysis of the genome of the unicellular cyanobacterium Synechocystip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S76734
A;Status: preliminary
A;Molicule type: DNA
A;Residues: 1-475 «KMN»
A;Reserveferences: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18646.1; PID:g165373
A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18646.1; PID:g165373
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable histidine decarboxylase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: 286500
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunger, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Atthers: Salzaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromsome 1 of the plant Arabidopsis.
A;Accession: E96500
A;Status: preliminary
A;Accession: B96500
A;Residues: 1487, SGNO
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A;Cross-references: GB:AE005173; NID:g7523682; PIDN:AAF63121.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 435;
          submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid D2024.
A; Reference number: 221488
A; Accession: T34200
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-435 a 6002>
A; Cross-references: EMBL:U41011; PIDN:AAA82288.1; CESP:D2024.3
A; Genetics:
A; Genetics: A; 57/3; 306/1; 398/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 36; Matches 5; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rRNA (guanosine-2'-O-)-methyltransferase (EC 2.1.1.-) - yeast (Saccharomyces cerevisiae)
NyAlternate names: mitochondrial large ribosomal RNA methylase; protein 04827; protein Y
Species: Saccharomyces cerevisiae
C;Dete: 29-Nov-1994 #sequence revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S48881; S07682; $67093
C;Accession: S48881; S07682; $67093
A;Situm-Connolly, K.; Mason, T.L.
Science 262, 1886-1889, 1993
A;Title: Functional requirement of a site-specific ribose methylation in ribosomal RNA.
A;Reference number: S48881; MUID:9409319; PMID:8266080
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C,Function:
A)Description: methyltransferase; required for formation of functional mitochondrial rib
C,Keywords: methyltransferase; mitochondrion
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A. Residues: 1-95 < STR>
A. Residues: 1-95 < STR
A. Residues: 1-95 < STR
A. Residues: 1-96 < STR
A. Residues: 1-96 < STR
A. Residues: 1-96 < STR
A. Residues: 1-97 < ST
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A,Status: nucleic acid sequence not shown; translation not shown
A,Status: nucleic acid sequence not shown; translation not shown
A,Residues: 1-412 ASIR>
A,Residues: Leferences: EMBL:L19947; NID:9431759; PIDN:AAA74564.1; PID:9431760
A,Residues: Lister and Library, December 1993
B,Struhl, K.
Nucleoide sequence was submitted to the EMBL Data Library, December 1993
B,Struhl, K.
A,Reference number: S07681; MUID:86093663; PMID:3001645
A,Reference number: S07681; MUID:86093663; PMID:3001645
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Cispecies: Caenorhabditis elegans
Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
CiAccession: T34200
Ribu, Z.; Gattung, S.
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                                                                                                                                                                                                                                                                                                                Length 338;
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100.0%; Score 31; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 31; DB 2; Best Local Similarity 100.0%; Pred. No. 28; Matches 5; Conservative 0; Mismatches 0
A,Experimental source: clone Y32B12B
C,Genetics:
A,Gene: CESP:Y32B12B.6
A,Map position: 5
A,Introns: 28/3; 61/1; 257/1
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A pathway: tyrocidine biosynthesis

C;Superfamily: acyl carrier protein homology; acetate-CoA ligase homology
C;Superfamily: acyl carrier protein homology; ACLI>
C;Keywords: carrier protein; phosphoprotein
C;Ckeywords: carrier protein homology ACLI>
C;S10-950/Domain: acetate-CoA ligase homology ACLI>
C;156-1987/Domain: acetate-CoA ligase homology ACLI>
C;253-3035/Domain: acetate-CoA ligase homology ACLI>
C;253-3035/Domain: acetate-CoA ligase homology ACLI>
C;253-3111/Domain: acetate-CoA ligase homology ACLI>
C;3043-3111/Domain: acetate-CoA ligase homology ACLI>
C;3043-3111/Domain: acyl carrier protein homology ACLI>
C;305-104/Domain: acyl carrier protein homology ACLI>
C;2505-2104/Domain: acyl carrier protein homology ACLIO>
C;2505-2106-207,3075,4110,5154,6197/Binding site: phosphopantetheine (Ser) (covalent)
                                                                                                                                                                                                      tyrocidine synthetase 3 - Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cipate: 02-8ep-2000 #sequence_revision 02-8ep-2000 #text_change 01-Dec-2000
Cidacession: 731076
Mirachiellus Marahiellus M.A.
J. Bacteriol. 179, 6843-6850, 1997
A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide seque A;Reference number: 220969; MUID:98012987; PMID:9352938
A;Reference number: 220969; MUID:98012987; PMID:9352938
A;Reference number: DAA
A;Residues: DAA
A;Residues: DAA
A;Residues: EMBL:AF004835; NID:92623770; PID:92623773; PIDN:AAC45930.1
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A;Residues: 1-118 a.CDA-
A;Cross-references: GB:MM9984
C;Croment: This protein recognizes a restricted idictype associated with antibodies speci
C;Comment: This protein recognizes a restricted idictype associated with antibodies speci
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin P;S-97/bomain: immunoglobulin homology <IMM>
F;S-97/bomain: immunoglobulin homology <IMM>
F;S-65/Region: complementarity-determining 1
F;S0-65/Region: complementarity-determining 3
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-May-1997
C;Accession. FQ0266
R;Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A;Titles: Sequence analysis of the variable region of a mouse gene encoding a monoclonal A;Reference number: PQ0265; MUID:92039046; PMID:1937027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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208 NYGVH 212
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C, Function:
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                                                                                                                                                RESULT 14
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A Residues: 1-697 < CON>
A Cross-references: EMBL:AP000265; NID:g1947147; PID:g1947154; PIDN:AAB52947.1; GSPDB:GN
A; Cross-references: Exain Bristol N2; clone C18E3
C; Genetics: CESP:C18E3.7
A; Gene: CESP:C18E3.7
A; Map position: 1
A; Introns: 12/2; 32/2; 72/1; 219/3; 315/2; 447/3; 666/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1465 <FUDE>
A; Residues: 1-1465 <FUDE>
A; Residues: 1-1465 <FUDE>
A; Residues: 1-1465 <FUDE>
B; Vinkemeder, U; Obermann, W; Weber, K.; Fuerst, D.O.
U; Cell Sci. 106, 319-330, 1993
A; Title: The globular head domain of titin extends into the center of the sarcomeric M b; Reference number: $42166; MUID:94095665; PMID:7505783
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hypothetical protein C18B3.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Homo sapiens (man)
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C,Accession: S43529, S42166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 2; Length 697; 100.0%; Pred. No. 58; ive 0; Mismatches 0; Indels
                                                                                                                                             100.0%; Score 31; DB 2; Length 482; 100.0%; Pred. No. 40; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Accession: T15179
R; Connell, M.; Maggi, L.
submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid C18E3.
A; Reference number: Z18304
A; Accession: T15179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                 A,Map position: 1
C,Superfamily: Klebsiella histidine decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiFuerst, D.O. submitted to the EMBL Data Library, October 1992 A; Reference number: $43529 A; Accession: $43529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A,Residues: 1-101, QR', 104-1465 <VIN>
A,Cross references: BMBL:X69089
C,Superfamily: skelemin
C,Keywords: skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165K protein, skeletal muscle - human
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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           A;Gene: F2J6.7
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Thu Oct 14 09:36:56 2004

1 NYGVH 5 |||:| 31 NYGIH 35

Search completed: October 6, 2004, 16:34:45 Job time : 8.26316 secs

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October 6, 2004, 16:34:15; Search time 31.1404 Seconds (without alignments) 51.669 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/NSO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT_NBW_PUB_Dep:*

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16: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB_Dep:*

17: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB_Dep:*

18: \cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB_Dep:*

18: \cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB_Dep:*

18: \cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB_Dep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1351062 segs, 321799191 residues
                                                                                                                              OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0. Maximum DB seq length: 2000000000
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31
1 NYGVH 5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

119 12 US-10-374-600-117 119 12 US-10-374-600-118 119 12 US-10-374-600-119 119 12 US-10-374-600-119 119 15 US-10-374-501-115 119 15 US-10-374-531-115 119 15 US-10-374-531-116 119 15 US-10-374-531-119 119 15 US-10-374-600-24 132 12 US-10-374-600-26 132 12 US-10-374-600-26 132 12 US-10-374-600-26 133 12 US-10-374-600-30 133 12 US-10-374-600-30 133 12 US-10-374-600-30 133 12 US-10-374-501-29 133 12 US-10-374-501-30 134 12 US-10-374-501-31 135 15 US-10-374-501-31 136 12 US-10-374-501-31 137 15 US-10-374-501-31 138 12 US-10-374-501-31 138 12 US-10-374-501-31 138 15 US-10-374-531-31 139 15 US-10-374-531-31 141 14 US-10-374-531-13	Sequence 117, App	118	119	Sequence 120, App	115	Sequence 116, App	117	118	119	120	24,	26,	Sequence 27, Appl	28,	29,	30,	24,	Sequence 26, Appl	27,	28,	29,	Sequence 30, Appl	ω	13	19	ω,	Sequence 13, Appl	19	47,	Sequence 47, Appl
	-10-374-600	US-10-374-600	US-10-374-600	US-10-374-600	US-10-374-531	US-10-374-531	US-1	us-	-Sn	ns-	us-	ns-	us-	us-	us-	us-	ns-	us-	ns-	US-	ns-	us-	us-	us-	us-	us-	US-10-374-531	US-10-374-531	9	11-
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	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
331 1000 1000 1000 1000 1000 1000 1000	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Sequence 26, Application US/09798689

Fublication No US20030103973A1

GENERAL INCPRARATION:

APPLICANT: Cockwell, Patricia

TITLE OF INVERTION: Combined with Radiation and Chemotherapy

TITLE OF INVERTION: Combined with Radiation and Chemotherapy

TITLE OF INVERTION WUMBER: US/09/799,689

CURRENT FILING DATE: 1994-09-22

FRIOR PILING DATE: 1995-09-22

FRIOR PELICATION NUMBER: 08/967,113

FRIOR PELICATION NUMBER: 08/967,113

FRIOR PELICATION NUMBER: 08/967,113

FRIOR PELICATION NUMBER: 08/967,113

FRIOR APPLICATION NUMBER: 08/106,804

FRIOR PELING DATE: 1995-06-07

FRIOR APPLICATION NUMBER: 08/126,041

FRIOR FILING DATE: 1994-02-10

1 NYGVH 5

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REGISTRATION NUMBER: 31,995
REPERBRICE/DOCKET UNBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                              ; HYPOTHETICAL: NO FRAGMENT TYPE: internal ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-374-600-1
                                                                                                                                                                 LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: S amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Broadway
CITY: New York
                                                                                             TELEFAX: (212) 425-5
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: US
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                                                                                                     Sequence 2, Application US/09996954B
; Sequence 2, Application US/0996954B
; Publication No. US20030157104A1
; GENERAL INFORMATION:
    APPLICANT: Maksal, Harlan W.
    APPLICANT: Maksal, Harlan W.
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    FILE REPRENCE: 11245-46665
    CURRENT APPLICATION NUMBER: US/09/996,954B
    CURRENT PILING DATE: 2001-11-30
    PRIOR PILING DATE: 09/314,028
    PRIOR FILING DATE: 08-13-1999
    PRIOR FILING DATE: 08-13-1999
    NUMBER: 09/312,284
    PRIOR FILING DATE: 08-14-1999
    NUMBER: PastSEQ for Windows Version 4.0
    SEQ ID NO 2
    LENGTH: 5
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Sequence 1, Application US/20030224001A1
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDER ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM comparible
COMPUTER: BM comparible
COMPUTER: Wordperfect
CURRENT APPLICATION NAMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION NAMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: AURHOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 31; DB 10; Length 5; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens-Rodent Chimera
US-09-996-954B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NYGVH 5
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       NYGVH 5
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US-10-374-600-1
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Gaps
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Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
ATTLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION: INHIBITING THE GROWTH OF TUMORS
Query Match 100.0%; Score 31; DB 12; Length 5; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENCY TARGET IN TOUGHTS OF THE CATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-MAR-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US/08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
```

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APPLICANT: Wisely Charles R
APPLICANT: Weekey, Charles R
APPLICANT: Weekey, Charles R
APPLICANT: Weekey, Charles R
APPLICANT: Leiby, Kevin R
APPLICANT: Leiby, Kevin R
APPLICANT: Leiby, Kevin R
APPLICANT: Leiby, Kevin R
APPLICANT: Goodean! Andrew
APPLICANT: Goodean! Andrew
APPLICANT: MOUGHAS A
TITLE OF INVENTION: DESCRICCIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: DESCRICCIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES: 2003-12-19
RIOR RELING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: PREVENCE NUMBER: US 09/602,871
PRIOR PILING
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Sequence 193465, Application US/10424599

PUBLICATION NO. US20040031072A1

SEQUENCE 19365, Application US/10424599

PUBLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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100.0%; Pred. No. 11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                          APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                         US-10-741-790-231
. Sequence 231, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
Barnes, Thomas S
Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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US-10-741-790-231
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APPLICANT: Sharp, John D
APPLICANT: March, Claries R
APPLICANT: Macre, Shan J
APPLICANT: Macre, Paul S
APPLICANT: Myers, Paul S
APPLICANT: Myers, Paul S
APPLICANT: Myers, Paul S
APPLICANT: Morela R
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                                                                                                                                                                                                                                       Length 5;
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100.0%; Score 31; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCatrly, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 231, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Sequence 218420, Application US/10424599
| Sequence 218420, Application US/10424599|
| Sequence 218420, Application No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPRENCE: 39-21(5323)=
| CURRENT APPLICANTON NUMBER: US/10/424,599|
| CURRENT PILING DATE: 2003-04-28|
| NUMBER OP SEQ ID NOS: 285684|
| SEQ ID NO 218420|
| LENGTH: 90
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(Sequence 281738, Application US/10424599)

(Sequence 281778, Application US/10424599)

(Publication No. US20040031072A1

(GENERAL INFORMATION)

(APPLICANT: La Rosa Thomas J

(APPLICANT: APPLICANT: A Roy of William Sept. CANT: APPLICANT: Cao Yongwei

(TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

(TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

(CURRENT APPLICANTION NUMBER: US/10/424,599

(CURRENT FILING DATE: 2003-04-28

(NUMBER OF SEQ ID NOS: 285684

(SEQ ID NO 281738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 31; DB 12; Length 93; Best Local Similarity 100.0%; Pred. No. 54; Matches 5; Conservative 0; Mismatches 0; Indels
                                              Query Match
100.0%; Score 31; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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US-10-424-599-218420
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US-10-424-599-281738
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100.0%; Pred. No. 53;
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Glycine max
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LOCATION: (1)..(9
  US-10-424-599-187665
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Sequence 187665, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cov variet David K
APPLICANT: Cao variet David K
APPLICANT: David William APPLICANT: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187665
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Formal Carlow No. US20040172684A1

GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
Cao, Yongwei
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APPLICANT:
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APPLICANT:
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE:
SEQ ID NOS: 63128
SEQ ID NOS: 63128
SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3478-058-Q6-K1-A9.pep
US-10-767-701-50344
                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_16723C.1.pep
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 193465
LENGTH: 65
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Matches 5; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                      ORGANISM: Glycine max
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Best Local Similarity
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US-10-424-599-187665
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                                                                                                                                                                                                                                                                                                                        Query Match
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RESULT 14
(S.10.374.600-115)
(S.10.374.600-115, Application US/10374600)
; Publication No. US20030224001A1)
; Publication No. US20030224001A1
; GENERAL INFORMATION:
    APPLICANT: ImClone Systems Incorporated, et al.
    TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS
; INTIBION INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPED Diskrete 3.5 inch 1.44 Mb storage
COMPUTER: IBM Compatible
SOFTWARE: Wordperfect
COMPUTER: IBM Compatible
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION APPRAR: US/89/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/89/9947
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 89/482,982
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAMM: Deborah A. SOMET'1119
RESISTRATION NUMBER: 131,995
ATTORNEY/AGENT NUMBER: 131,995
RESISTRATION NUMBER: 131,995
REPREMENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 31, DB 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10374600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 425-5288 INFORMATION FOR SEQ ID NO: 115:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212)
TELEFAX: (212) 4:
. 5; Conservative
                                                                            31 NYGVH 35
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                                         1 NYGVH 5
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US-10-374-600-116
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 116;
68;
                                                                                                                                                 Sequence 4, Application US/10435299
Publication No. US20040052783A1
Publication No. US20040052783A1
Publication No. US20040052783A1
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
FILE REPRENCE: 05882-0175-CNUS04
CURRENT APPLICATION NUMBER: US/10/435,299
CURRENT FILING DATE: 2003-05-09
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PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 100-10-18
PRIOR PLILING DATE: 1995-03-01
PRIOR APPLICATION NUMBER: US 07/859,583
PRIOR PILING DATE: 1992-03-27
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 4
IENCIP DO 4
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
                                                        14 NYGVH 18
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                                                                               NUMBER OF SEQUENCES: 120
CORRESPONDENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
CITY: New York
STREET: One Broadway
CITY: New York
STREET: One Broadway
CONDUTRY: US
ZIP: 10004
ZIP: 10004
ZIP: 10004
COMPUTER READABLE FORM:
MCDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER READABLE FORM:
MCDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OCHPUTER: IBM compatible
OCHPUTER: IBM compatible
OFERATION SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRING DATE: 15-Feb-2003
CLIANG DATE: 15-Feb-2003
CLIANG DATE: 19-MAR-1996
APPLICATION NUMBER: US (08/973,065C
FILING DATE: 19-MAR-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
APTORNEY/ACRY INFORMATION:
NAME: Deborah A. SOMERVILLE
REFERENCE/DOCKET NUMBER: 11245/46003
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-5286
INPORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 31; DB 12; Length 119; Best Local Similarity 100.0%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 0; Indels 0
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-374-600-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 NYGVH 35
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Search completed: October 6, 2004, 17:09:02 Job time : 34.1404 secs

sequence 4950, Applagemence 68, Appl Sequence 2, Appli Sequence 9, Appli Sequence 9, Appli Sequence 4, Appli Sequence 3752, Applagemence 2, Appli Sequence 66, Appli Sequence 7985, Appli Sequence 5717, Appli Sequence 571

42, Appl 53, Appl 18, Appl 24, Appl 5242, Ap

Sequence Sequence Sequence Sequence Sequence

October

Run on:

Perfect score:

Sequence:

Scoring table:

Minimum DB seq Maximum DB seq

Database

Result

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RESULT 1
US-08-397-411-3

1 US-08-397-411-3

1 Sequence 3, Application US/08397411

2 Fatent No. 6129914

3 General Normation:
APPLICANT: Wainer, George
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun

TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: Bispecific Antibody Effective
CORRESPONDENCE ADDRESS:
ADDRESSEE: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: One Market Plaza, Steuart Tower, Suite 2000

STREET: One Market Plaza, Steuart Tower, Suite 2000

STREET: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTE: 74105
COMPUTE: 74105
COMPUTE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: US/08/397,411
FILING DATE: US/08/397,411
PRICATION NUMBER: US/08/397,411
APPLICATION NUMBER: US/08/397,411
APPLICATION NUMBER: US/08/397,411
APPLICATION NUMBER: US/08/397,411
TELEPHONE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMALT WIlliam M.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REGISTRATION INFORMATION:
TELEPHONE: 415-326-2407
TELEPHONE: 415-326-2407
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
                       US-09-328-352-4950

US-09-456-090A-68

US-08-480-053-2

US-08-401-889-9

US-08-417-264-9

US-09-417-264-9

US-09-417-264-9

US-09-134-0010-3752

US-09-134-0010-3752

US-09-134-864-45

US-09-903-486-53

US-09-903-456-53

US-09-903-456-54

US-09-903-456-54

US-09-903-456-54

US-09-134-0000-5242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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     Sequence 14, Appl
Sequence 47, Appl
Sequence 20, Appl
Sequence 27, Appl
Patent No. 5455030
Patent No. 5455030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7, Appli
5340, Ap
2, Appli
1, Appli
1, Appli
39, Appl
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Sequence 6, Appli
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Sequence 4, Appli
                                                                                                                                                                                2004, 16:24:54 ; Search time 8.85965 Seconds (without alignments) 29.135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ssued_Patents_AA:*
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-397-411-4
US-08-38-749A-14
US-09-903-456-47
US-09-145-828A-20
US-09-145-828A-20
5455030-13
5455030-13
5455030-13
US-08-397-411-7
US-08-397-411-7
US-08-134-000C-5340
US-08-211-430-2
US-08-761-136-1
US-08-761-136-1
US-09-761-136-1
US-09-761-136-1
US-09-761-274-8
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US-09-240-274-20
US-09-240-274-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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31
1 NYGVH 5
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Match Length
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100.0%; Score 31; DB 3; Length 116; 100.0%; Pred. No. 24; cive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 5; Conservative

Sequence Sequence

US-09-240-274-16 US-09-240-274-147 US-09-240-274-148

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Query Match
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A FILING DATE: 07-UW-1995 CLASSIFICATION: 536 ATTOWNEY/AGENT INFORMATION: NAME: SAVEREIDE, PAUL B. REGISTRATION NUMBER: 36,914 REPRENCE/DOCKET UNMBER: 36,914 REPRENCE/DOCKET UNMBER: 0508.008 TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 601-2585
INTELLECTUAL PROPERTY - R440, PO BOX 8097
                                                                                 ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 47, Application US/09903456
Patent No. 6677145
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-483-749A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                       EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 NYGVH 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NYGVH 5
                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-903-456-47
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LENGTH: 141
                                                                   COUNTRY:
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Patent No. 605454
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     Sequence 4, Application US/08397411

Patent No. 6129914

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OF THE CAPITION:
GENERAL OF THE CAPITION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
BISPECIFIC Antibody Effective to Treat
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 31; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Townsend and Townsend and Crew
F: One Market Plaza, Steuart Tower, Suite 2000
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REDDABLE FORM:
MEDIUM TYPE: Floppwish
MEDIUM TYPE: Floppwish
COMPUTER: IBM PC compatible
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-397-411-4
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                                                                      31 NYGVH 35
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                              1 NYGVH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-483-749A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ca
                                                                                                                                         RESULT 2
US-08-397-411-4
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: (141) ...(141)
, OTHER INFORMATION: Xaa = Unknown or Other at position 141
US-09-903-456-47
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Monardi Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Heang, Yung-Shang
APPLICANT: Pereira, Suzette L.
ITILE OF INVENTION: ELDOMGASE GENES AND USES THEREOF
FILE REPERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 2000-07-24
PRIOR PRILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
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RESULT 8
5455030-15
FACENT NO. 5455030
APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
FOLYPEPTIDE BINDING MOLECULES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-ARR-1993
PRICR APPLICATION NUMBER: 512,910
FILING DATE: 25-ARR-1990
APPLICATION NUMBER: 52,110
FILING DATE: 10-SEP-1987
FILING DATE: 10-SEP-1987
FILING DATE: 01-SEP-1986
                                                                                                                                     FPECHON STANDAR, KOBERT C., BIRD, ROBERT E., HARDMAN, KARL TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN FOLYPEPTIDE BINDING MOLECULES STANDER BEDIED BINDING MOLECULES STANDER OF SEQUENCES: 24

CURRENT APPLICATION DATA:

PILING DATE: 1-APR-1993

PRIOR APPLICATION NUMBER: 512,910

PILING DATE: 25-APR-1990

APPLICATION NUMBER: 29,617

FILING DATE: 02-SEP-1987

APPLICATION NUMBER: 92,110

FILING DATE: 02-SEP-1987

APPLICATION NUMBER: 92,110

FILING DATE: 02-SEP-1987

FILING DATE: 02-SEP-1987

FILING DATE: 01-SEP-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/09903456
Patent No. 6677145
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; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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NYGVH 67
                                                                      RESULT 7
5455030-13
;Patent No. 5455030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;SEQ ID NO:13:
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LENGTH: 239
5455030-13
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mikerji, Pradig
APPLICANT: Mikerji, Pradig
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: APPLICANT: Stephen
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.01
CURRENT APPLICANTON NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FARTSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-US-1903-426-27

Sequence 27, Application US/09903456
Fatent No. 6677145
GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Heang, Yeradip
APPLICANT: Heang, Yeragip
APPLICANT: Heang, Yang-Sheng
APPLICANT: Heang, Yang-Sheng
APPLICANT: Honney, Yang-Sheng
APPLICANT: Honney, Yang-Sheng
APPLICANT: Honney, Yang-Sheng
APPLICANT: Honney, Yang-Sheng
CURRENT FILE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2000-07-24
PRIOR PELLORICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR PILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
                                                                                                                                                                                           Sequence 20, Application US/09145828A
Patent No. 6403349
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Best Local Similarity 100.
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TYPE: PRT ORGANISM: Homo sapiens

US-09-145-828A-20

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TYPE: PRT
CORGANISM: Homo sapiens
US-09-903-456-27

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RESULT 12
US-09-134-000C-5340
; Sequence 5340, Application US/09134000C
     STRANDEDNESS: single
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                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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TELEFAX: 4
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) Sequence 6, Application US/08397411
) Patent No. 6129914
) GENERAL INFORMATION:
APPLICANT: Gingrich, Roger
APPLICANT: Link, Batan
APPLICANT: Link, Batan
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 4; Length 265; 100.0%; Pred. No. 55; 0; Indels cive 0; Mismatches 0; Indels
APPLICANT: Mukerji, Pradip
APPLICANT: Lecnard, Amanda Eun-Yeong
APPLICANT: Lecnard, Amanda Eun-Yeong
APPLICANT: Heung, Yung-Sheng.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
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APPLICATION NUMBER: US 07/859,583
PILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTATION NUMBER: 30,223
REFERRICE/DOCKET NUMBER: 011823-004;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-903-456-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 NYGVH 174
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STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 64
LENGTH: 265
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                                                DB 3; Length 273;
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COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
TITING DATE: 01-MAA-1995
                                                   100.0%; Score 31; DB 100.0%; Pred. No. 57;
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Smith, William M. REGISTRATION NUMBER: 30,23 REFERENCE/DOCKET NUMBER: 01. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 446 amino acids
amino acid
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Best Local Similarity 100.v
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-326-2422
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-6
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RESULT 15
US-09-576-967-1
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Patent No. 5763166

GENERAL INFORMATION:
PAPLICANT:
TITLE OF INVENTION: X CHROMOSOME LINKED KALLMANN SYNDROME, CORRESPONDING
TITLE OF INVENTION: X CHROMOSOME LINKED KALLMANN SYNDROME, CORRESPONDING
TITLE OF INVENTION: PEPTIDE SEQUENCES, DIAGNOSTIC APPLICATIONS.
NUMBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,430
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/059,778
PRIOR APPLICATION NUMBER: US 60/059,778
NUMBER OF SEQ ID NOS: 6812
SOFWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 4; Length 505
Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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Patent No. 6121231
GENERAL INFORMATION:
APPLICANT: PETIT, CHRISTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL LINE: foetal brain cell
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                                                                                                                                                                                                                                                                                                                                                                                                                     96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 680 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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195 NYGIH 199
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APPLICANT: HARDELIN, JEAN-PIERRE
APPLICANT: SARAILH, CATHERINE
APPLICANT: ROUGON, GENEVIEVE
APPLICANT: ROUGON, GENEVIEVE
APPLICANT: AROUN, OLIVIER
APPLICANT: ARDOUN, OLIVIER
APPLICANT: ARDOIN, SERVENCENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 $. JEFFERSON DAVIS HIGHWAY, SUITE 400
GTTY: ARLINGTON
GTTY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND TREATMENT WITH TREATMENT OF RETINAL, RENAL, NEUROMAL
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 2.38+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,136
FILING DATE: 06-DEC-1996
ATTONNEY/AGENT INPORMATION:
NAME: OBLOW, NORMAN F:
REGISTRATION NUMBER: 660-112-0
FELERMONE 703-413-3000
TELERMONE 703-413-3000
TELERMA: 703-413-3000
TELERMA: 703-413-3000
TELERMA: 703-413-3000
SEQUENCE CHARACTERISTICS:
TENTAL CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PETIT, CHRISTINE
SOUSSI-YMATICCCTAS, NADIA
HARDELIN, JEAN-PIERRE
SARAILH, CATHERINE
ROUGON, GENEVIEVE
LEGOUIS, RENAUD
ARDOUIN, OLIVIER
MAZIE, JEAN-CLAUDE
TITLE OF INVENTION: USE OF KAL PROTEIN ANI
AND NEURAL INJURY
AND NEURAL INJURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/09576967; Patent No. 6548475; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.8%;
Best Local Similarity 80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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us-09-635-974a-2.rai

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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
STATE: VA
COUNTY: AALINOTON
CONFUTER: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/576,967
FILING DATE: 24-MAY-200
FILING DATE: 24-MAY-200
FILING DATE: 34-MAY-200
FILING DATE: 34-MAY-200
FILING DATE: 44-MAY-200
FIL
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Search completed: October 6, 2004, 16:36:30 Job time: 9.85965 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 16:23:59 ; Search time 6.31579 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-10 25 1 ASESIS 6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 1008
Maximum Match 1008
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hain V	hain	hain	Ig kappa chain pre	hain	hypothetical prote	pgal protein - Asp	l pro	ы	phosphatidylinosit	microtubule-vesicl	restin - human	hypothetical prote	cal	heli	probable membrane	threonyl-tRNA synt	zinc finger protei	zinc finger protei	hypothetical prote)le		IgA-specific metal	probable sensory t	riae-ass	CDA peptide synthe	cal	netical	netical
QI	PH1082	KVRB38	C30502	KVMSL7	PN0445	E90552	S17980	T37740	T50143	JC4889	A43336	59	16	8	T13299	9	55	39	39	30	14	55	33	검	15	T36249	26	46	85
Length DB	7	2	90	15	28	248 2	68	9	32	188	92	427	04	49	43	91	35	83	85	91	57	93	532	639	70	670	16	40	11
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hypothetical prote	hypothetical prote	chaperone protein	outer membrane pro	pilQ protein - Nei	pilus secretin NMA	suppressor of sabl	hypothetical prote	hypothetical prote	Ig light chain V r	Ig kappa chain V r					
867571	G86713	AB0824	A37051	570838	A81985	T13855	T30037	T24490	PH1080	S78488	516827	S34086	S16840	534084	\$34083
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583	584	919	711	720	761	1473	1539	2251	69	86	98	98	86	87	87
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95.	o									٠.					
92		23	23	23	23	23	23	23	22	22	22	22	22	22	22

ALIGNMENTS

RESULT 1
PH1082
Ig light chain V region (clone 165.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C,Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 21-Jan-2000
C, Accession: PH1082
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
f. Exp. Med. 176, 761-779, 1992
A, Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B
A; Reference number: PH0971; MUID: 92381444; PMID:1512540
A; Accession: PH1082
A;Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A;Residues: 1-87 <til></til>
A; Experimental source: B cell, strain [NZB x NZW]F1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoqlobulin
F;6-80/Domain: immunoglobulin homology <imm></imm>
Query Match 100.0%; Score 25; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 8.2; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OV TASES1S 6

ASESIS 6 ò g

41

Ighapa chain V region (3381) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 21-Jan-2000
C;Accession: A01953
R;Margolies, M.N.; Cannon III, L.B.; Strosberg, A.D.; Haber, E.
Proc. Natl. Acad. Sci. US.A. 72, 2180-1284, 1975
A;Title: Diversity of light chain variable region sequences among rabbit antibodies elic A;Reference number: A93799; MUID:75176905; PMID:1094456
A;Accession: A01953
A;Accession: A01953
A;Accession: A01953
A;Molecule type: protein
A;Residues: 1-92 cMAR>
C;Comment: This chain was obtained from antibody to type III pneumococci and was isolate C;Comment: This chain heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer
F;16-90/Domain: immunoglobulin homology cIMM>
F;23-88/Disulfide bonds: #status predicted

ö Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 6; Conservative 0; Mismatches 0; Indels

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pgal protein - Aspergillus niger
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C;Superfamily: polygalacturonase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-128 <KAL>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <KUR>
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Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-368 <BUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ASESIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ASESIS 16
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A;Genetic code: SGC3
                                                                                                                                                       A; Accession: PN0445
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A,Residues: 1-115 <PEC>
A,Cross-references: GB:V01564; GB:J00574; NID:g51718; PIDN:CAA24884.1; PID:g758153
A,Note: the sequence was determined from the germline gene
A;Note: there appear to be two possible splice junctions at the 3' end of the intron; th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor V region (L7) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999
C;Accession: A01925
R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A;Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequence number: A93259; MUID:81220975; PMID:6264318
A;Accession: A01925
                                                                                                                        RESULT 3
C30502
C30502
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C; Date: 03.002
R; Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A; Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 184, A; Ccession: C30502
A; Status: preliminary
A; Mccession: C30502
A; Status: preliminary
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-108 <br/>
A)Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072<br/>
A;Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072<br/>
C)Superfeamily: immunoglobulin V region; immunoglobulin homology<br/>
C;Keywords: heterotetramer; immunoglobulin<br/>
F;16-90/Domain: immunoglobulin homology <IMM>
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-21/Product: Ig kappa chain V region (L7) #status predicted
F;36-110/Domain: immunoglobulin homology <IMM>
F;36-110/Domain: immunoglobulin predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 25; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels
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PN0445
Ig kappa chain precursor V-I region - human (fragment)
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                                               25 ASESIS 30
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ASESIS
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hypothetical protein MYPU 3250 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C,Species: Mycoplasma pulmonis
C,Species: Mycoplasma pulmonis
C,Fate: 24 May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C,Accession: E90552
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A,Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmon, A,Reference number: A99512; MUD:21267165; PMID:11353084
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession. 817980
R;Bussink, H.J.D.; Brouwer, K.B.; de Graaff, L.H.; Kester, H.C.M.; Visser, J.
Curr. Genet. 20, 301-307, 1991
A;Title: Identification and characterization of a second polygalacturonase gene of Asperg
A;Reference number: 817980; WUID:92035101; PMID:1934135
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #text_change 21-Jan-2000
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0445
B;Kaluza, B; Betzl, G; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymeras
A;Reference number: PN0444; WUID:93138402; PMID:1339379
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A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               A)Cross-references: GB:L02347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 2; Length 128; 100.0%; Pred. No. 13; 0; Indels ive 0; Mismatches 0; Indels
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Accession: PC4889
A; Accession: Occasion of a human placenta inositol 1,3,4,5-terrakisphosphate, A; A; Deserver, A.L.; Deserver, A; Title: Cloning and expression of a human placenta inositol 1,3,4,5-terrakisphosphate, A; Accession: UC4889; MUID:96332436; PMID:8769125
A; Accession: UC4889
A; Accession: C4889
A; Residues: DNA
A; Residues: L188 CADA-A; Residues: DNA
A; Residues: L188 CADA-A; Residues: DNA
A; A; DNA
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C;Species: Homo sapiens (man)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Nov-1999
C;Accession: $22695; $19853
C;Accession: $22695; $19853
C;Accession: $22695; $19853
EMBO J: 11, 2103-2113, 1992
EMBO J: 11, 2103-2113, 1992
A;Title: Restin: a novel intermediate filament-associated protein highly expressed in th A;Reference number: $22695; WUID:92289675; PMID:1600942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microtubule-vesicle linker CLIP-170 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: A43336
R;Pierre, P.; Scheel, J.; Rickard, J.E.; Kreis, T.E.
Cell 70, 897-900, 1992
A;Title: CLIP-170 links endocytic vesicles to microtubules.
A;Reference number: A43336; MUID:92405160; PMID:1356075
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A;Molecule type: mRNA
A;Residues: 1-1392 ePIE>
A;Cross-references: GB:M97501; NID:g180621; PIDN:AAA35693.1; PID:g180622
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A,Residues: 1-1427 <BLL>
A,Cross-references: EMBL:X64838; NID:g35998; PIDN:CAA46050.1; PID:g35999
C,Keywords: cytoskeleton
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Matches 6; Conservative
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192 ASESIS 197
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RRIEGET, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

RRIEGET, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

A; Reference number: 221743

A; Reference number: 221743

A; Reference number: 221740

A; Reference number: 221740

A; Ratus: preliminary; translated from GB/EMBL/DDBJ

A; Ratus: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-649

A; Residues: 1-649

A; Experimental source: strain 972h-; cosmid c167

A; Experimental source: strain 972h-; cosmid c167

A; Gonetics:
A; Gonetics:
A; Map position: 1
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R;Hamiin, N.; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999
A;Reference number: Z25043
A;Accession: T50143
A;Accession: T50143
A;Accession: T50143
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Rolocule type: DNA
A;Residues: 1-732 <HAM>A;Residues: 1-732 <HAM>A;Residues: BRBL:AL132798; PIDN:CAB60694.1; GSPDB:GN00066; SPDB:SPAC222.02c
A;Experimental source: strain 972h(-); cosmid c222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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                                                                                             Gaps
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        Query Match 100.0%; Score 25; DB 2; Length 368; Best Local Similarity 100.0%; Pred. No. 42; Matches 6; Conservative 0; Mismatches 0; Indels
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.larity 100.0%; Pred. No. 92;
Conservative 0; Mismatches 0; Indels
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A;Gene: SPAC1687.22c; SPDB:SPAC222.02c
A;Map position: 1
A;Introns: 656/2; 711/1
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Search completed: October Job time: 9.31579 secs
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Matches 5,
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                                                                                                                                                                                                                                                  hypothetical protein Vng0091c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
S;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
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A,Molecule type: DNA
A,Residues: 1-304 <STO>
A,Cross-references: GB:AE004437; NID:g10579742; PIDN:AAG18722.1; GSPDB:GN00138
C,Genetics:
A,Gene: VNG0091C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted to the EMBi Data Library, October 1995
A;Reference number: 219129
A;Reference number: 219129
A;Accession: 179485
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-349 <WILL.
A;Cross-references: EMBL: 254327; PIDN:CAA91121.1; GSPDB:GN00020; CESP:C26D10.3
A;Experimental source: clone C26D10
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C;Species: Streptococcus phage phi-01205
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19485
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100.0%; Score 25; DB 2; Length 1427; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels 0
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Pred. No. 78;
1; Mismatches (
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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A,Map position: 2
A,Introns: 47/3; 197/1; 277/3
                                                   6; Conservative
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    Query Match
Best Local Similarity
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T13299
                                                   Matches
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C; Accession: T13299
R; Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.
Microbiology 143, 3417-3429, 1997
A; Title: Sequence analysis and characterization of phi 01205, a temperate bacteriophage
A; Reference number: 217654; MUID: 98048466; PMID: 9387220
A; Accession: T13299
A; Status: translated from GB/EMBL/DDBJ
A; Residus: translated from GB/EMBL/DDBJ
A; Residus: 1-443 < STA>
A; Residues: 1-443 < STA>
A; Residues: 1-443 < STA>
A; Experimental source: host Streptococcus thermophilus strain CNRZ1205
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6, 2004, 16:34:54

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5.1.6	Compugen
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GenCore ve	(c) 1993
	Copyright

OM protein - protein search, using sw model

6, 2004, 16:20:48 ; Search time 75.7895 Seconds (without alignments) 55.921 Million cell updates/sec October Run on:

US-09-635-974A-4 88 1 VIWSGGNTDYNTPFT 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp201s:*
5: geneseqp2013s:*
7: geneseqp2003as:*
7: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw08940 CDR2 from	Aav59312	Aab3795	Aau77785	Aaw08939 CDR2 from	Aaw08953 Heavy	Aaw08950	Aaw08952		Aaw08954 Heavy	Aaw08947 Heavy		Aaw08942	3 Single	Aaw05135	Aaw05140 scFv2(225	Aaw05139 SCFv2 (FRP	Aaw05141 scFv2(FRP	Aae17798 E. coli	Aae17793 Escherich	Aau72856		Add25438	Aar25728	
ID	AAW08940	AAY59312	AAB37953	AAU77785	AAW08939	AAW08953	AAW08950	AAW08952	AAW08951	AAW08954	AAW08947	AAW08944	AAW08942	AAW05133	AAW05135	AAW05140	AAW05139	AAW05141	AAE17798	AAE17793	AAU72856	AAU72848	ADD25438	AAR25728	7470744
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	。	79.5	σ.	73.9	•	73.9	•	720
Score	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	70	70	65	65	65	65	u
Result No.		71	٣	4	ເກ	w	7	α	σ	10	11	12	13	14	15	16	1,1	18	1.9	20	21	22			c

Aab69675 Murine mi	Aab69660 Human Lay	Aau72846 Anti-NKG2	Aau72854 Anti-NKG2	Aar06355 Peptide c	Aab69656 Murine mi	Aar56235 h66-118/h	Aar56236 166-111/1	Aar14704 Vl-Lab-Vh	Aar14789 Vl-Lab-Vh	Aar14695 Vl-Lab-Vh	Aar14696 Vl-Lab-Vh	Aar14697 Vl-Lab-Vh	Aar14694 Vl-Lab-Vh	Aar14702 Vh-Lab-Vl	Aar14703 Vh-Lab-Vl	Aar14699 Vh-Lab-Vl	Aar14700 Vh-Lab-Vl	Aar14701 Vh-Lab-Vl	Aar15690 Vl-Lab-Vh
AAB69675	AAB69660	AAU72846	AAU72854	AAR06355	AAB69656	AAR56235	AAR56236	AAR14704	AAR14789	AAR14695	AAR14696	AAR14697	AAR14694	AAR14702	AAR14703	AAR14699	AAR14700	AAR14701	. AAR15690
ი	9	0	0	7	38	19	23	28	28	35	35	35	35	36	36	36	36	236 2	36
73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9									73.9	
رى س	Ŋ	ري ک	S	S	Ŋ	Ŋ	S.	c)	Ŋ	S	S	2	D.	ري د	ß	D.	r.	65	Ŋ
26	27	28	29	30	31	32	33	34				38			41	42	43	44	45

ALIGNMENTS

AAW08940 standard; peptide; 16 AA. 18-SEP-1997 (first entry) AAW08940; RESULT 1 AAW08940

CDR2 from heavy chain variable region of reshaped H225 antibody.

Complementarity determining region 2; CDR2; heavy chain; variable region; reshaped; human; monoclonal; antibody; H225; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate.

Homo sapiens.

WO9640210-A1.

19-DEC-1996,

96WO-US009847. 07-JUN-1996; 95US-00482982. 95US-00573289. 07-JUN-1995; 15-DEC-1995;

(IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.

Saldanha JW; Goldstein NI, Giorgio NA, Jones ST,

WPI; 1997-051897/05.

Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.

Claim 1; Page 83; 112pp; English.

The present peptide is the complementarity determining region 2 (CDR2) from the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, which is specific for the human epidemial growth factor (EGP) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle inhibitor

Sequence 16 AA;

Anti-EGFR monoclonal antibody H chain V region CDR2 peptide sequence.

(first entry)

L2-MAR-2001

99US-00312284.

14-MAY-1999; 13-AUG-1999;

23-NOV-2000

(IMCL-) IMCLONE SYSTEMS INC

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Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                               Refractory tumour growth inhibition, epidermal growth factor receptor, EGFR antagonist, cancer, squamous cell carcinoma, anti-EGFR antibody; complementarity determining region, CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 13; 31pp; English
AAB37953 standard; protein; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000; 2000WO-US011756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-016160/02
N-PSDB; AAC83236.
                                                                                                                                                                                                                                                                                                                            WO200069459-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waksal HW;
                                            AAB37953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the hypervariable region CDR2 (complementarity determining region 2) of the heavy chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to the patient makes the tumour more susceptible to radiotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypervariable region, complementarity determining region, CDR, tumour; single chain antibody, growth inhibitor; human, tumourigenesis; therapy, protein receptor tyrosine kinase, heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.
                                                                     Gaps
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                        Length 16;
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100.0%; Pred. No. 2.9e-07;
iive 0; Mismatches 0; Indels
                                                                     0; Indels
                      100.0%; Score 88; DB 2; I
100.0%; Pred. No. 2.9e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain hypervariable region, CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 14; 31pp; English.
                                                                                                                                                                                                                                                                                  AAY59312 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00079612.
98US-0085613P.
98US-00206138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US010741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND.
                                                                                                                    1 VIWSGGNTDYNTPFT 15
                                                                                                                                                              VIWSGGNIDYNIPFI 15
                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2000 (first entry)
  Saleh MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-062440/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ48626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
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15-MAY-1998;
07-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9960023-A1
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                                                                                                                                                                                                                                                                                                                                AAY59312;
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This invention relates to a method for inhibiting the growth of refractory tumours that are stimulated by a ligand of epidermal growth the acctor receptor (EGRN) in human patients. The method involves treating the patient with a combination of EGRN/human EGF-1 (HERRI) antagonist, optionally with a chemotherapeutic agent or radiation. The antagonist can be for example a chimeric anti-EGRN monoclonal antibody, CZS2. The EGRN/HERI antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, spleen, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence represents the heavy chain variable region complementarity determining region 2 amino acid sequence of the chimeric anti-EGFR monoclonal antibody CZS5 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 88; DB 4; Length 16; 1 Similarity 100.0%; Pred. No. 2.9e-07; 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU77785 standard; peptide; 16 AA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvention
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AAU77785
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ZXEXEXEX
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Mouse; heavy chain; antibody; hyperproliferative disease;

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Gaps ; 0

> 1 VIWSGGNTDYNTPFT 15 VIWSGGNTDYNTPFT 15

> > RESULT 3 AAB37953

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Conservative

Local Similarity les 15; Conser

Best Loca Matches

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Disclosure; Page 12; 28pp; English
                                                                                                                                                                                                                                                                                       AAW08939 standard, peptide, 18 AA.
                                                  09-AUG-2001; 2001WO-US041647;
                                                           09-AUG-2000; 2000US-00635974.
                                                                     (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                     1 VIWSGGNIDYNIPFI 15
                                                                                                                                                                                                                                                                                                          18-SEP-1997 (first entry)
                                                                                                                                                                                                                                      Local Similarity 100.
ses 15; Conservative
                                                                                         WPI; 2002-257423/30.
                                                                                              N-PSDB; ABK11441
                             WO200211677-A2.
                                                                                                                                                                                                                       Sequence 16 AA;
                                                                                                                                                                                                             he invention
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   WO9640210-A1
                                       14-FEB-2002
                                                                               Teufel T;
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                  AAW08939,
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Matches
                    Mus
                                                                                                                                                                                                                                                                             RESULT 5
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The present peptide is the complementarity determining region 2 (CDR2) from the heavy chain variable region of the reshaped human monoclonal antibody (Wab) H225, which is specific for the human epidermal growth factor (EGF) receptor. The Mab, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell
                                                                                                                                                                                                                                                                               Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain; reshaped; monoclonal; antibody; 225RD; human; papidermal growth factor; BGF; receptor; inhibition; growth; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
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                                                                                                                                                                                                         Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 88; DB 2; L
100.0%; Pred. No. 3.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable region of 225RD antibody.
                                                                                                                                                                                                     Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50. .65
/label= CDR_2
66. .97
/label= framework_3
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label= framework_1
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109. .119
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW08953 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 83; 112pp; English.
                                                                                                                                            (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                    95US-00482982.
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/label= CDR_1
                                                 96WO-US009847.
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18s 15; Conservative
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                                                                                                                                                                                                                                            WPI; 1997-051897/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
                                               07-JUN-1996;
                                                                                    07-JUN-1995;
15-DEC-1995;
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            19-DEC-1996,
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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AAW08953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGF) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the antagonist and phototherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal growth factor receptor (EGFR) antagonist by inhibiting EGFR /HERI phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic stimulated by a ligand of a member of the EGF family of receptor. This sequence represents the mutine anti-EGF 255 antibody heavy chain (Wh) hypervariable region (CDR2) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity determining region 2; CDR2; heavy chain, variable region; reshaped; human; monoclonal; antibody; H225; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate.
                                                                                                                                                                                                                                                                                                                                                                                                           Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR2; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDR2 from heavy chain variable region of reshaped H225 antibody.
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Gaps . 0 tumour; cell;

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Goldstein NI,
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                                             07-JUN-1995;
15-DEC-1995;
                          07-JUN-1996;
         19-DEC-1996
                                                                                                                                                                                                                                                                                           Query Match
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                          The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHD. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour calls, especially late stage prostatic tumour calls in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                             Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                           100.0%; Score 88; DB 2; Length 119; 100.0%; Pred. No. 2.7e-06; ive 0; Mismatches 0; Indels
                                                                                                          Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain variable region of 225RA antibody.
                                                                                                          Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98. .108
/label= CDR_3
109. .119
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66. .97 __/label= framework_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .30
/label= framework_1
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                                                                                                                                                                                                                                                                                                                                                                                                       AAW08950 standard; protein; 119 AA.
                                                                                                                                                                            Claim 30; Fig 22; 112pp; English.
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/label= framewords0. .65
/label= CDR_2
                                                                                       (MRCC-) MRC COLLABORATIVE CENT
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/label= CDR_1
                              96WO-US009847.
                                                 95US-00482982.
                                                                              (IMCL-) IMCLONE SYSTEMS INC.
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                             WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                            Sequence 119 AA;
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                              07-JUN-1996;
                                                 07-JUN-1995;
15-DEC-1995;
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                                                                                                                                                                                                                                                                                  Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
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                                                                                                                                                                                           Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain variable region of 225RC antibody.
                                                                                                                                                                                        Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36. .49
/label= framework_2
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/label= CDR_2
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/label= framework_1
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                                                                                                                      (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
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/label= CDR_1
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96WO-US009847.
                                           95US-00482982.
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/label= CI
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/label= f
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es 15; Conservative
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The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHB. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
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                                                                                                                                                                                                                                Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 119;
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                                                                                                                                                                          Saldanha JW;
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100.0%; Pred. No. 2.7e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                     Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36. .49
/label= framework_2
50. .65
/label= CDR_2
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1. .30
/label= framework_1
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/label= framework_4
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                                                                                                                                                                                                                                                                               Claim 30; Fig 22; 112pp; English.
                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
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/label= CDR_3
109. 110
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/label= CDR_1
                                              96WO-US009847
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95US-00573289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 119 AA;
                                                                                                                                                                       Goldstein NI,
                                          07-JUN-1996;
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15-DEC-1995;
              19-DEC-1996
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                                                                                                                                                                                                                      Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 88; DB 2; Length 119; 100.0%; Pred. No. 2.7e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                           Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region of 225RB antibody.
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//abel= CDR_1

36...49

//abel= framework_2

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//abel= CDR_2

66...97

//abel= framework_3

98...108

//abel= framework_3
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/label= framework 1
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                                                                                                              (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT
                                                                  95US-00482982,
95US-00573289,
                                      96WO-US009847
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Matches 15; Conservative
                                                                                                                                                                                            WPI; 1997-051897/05.
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                                                                07-JUN-1995;
15-DEC-1995;
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The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RHA. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
for inhibiting tumour growth, esp. of late stage prostatic tumour.
                        Claim 31; Fig 20; 112pp; English.
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N-PSDB; AAT49343.
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                                                                                                                                Saldanha JW
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                                                                                                                                 Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW08947 standard; protein; 138 AA.
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95US-00573289
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                  Sequence 119 AA;
                                                                                                                                   Goldstein NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1997
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                                         07-JUN-1996;
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                                                                         15-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric.
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Length 138;
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100.0%; Score 88; DB 2; L
100.0%; Pred. No. 3.2e-06;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain variable region of C225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example IV; Fig 16; 112pp; English.
                                                                                                                                                                                                                                                                                                                                           AAW08944 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-00482982.
95US-00573289.
                                                                                                                             1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                       69 VIWSGGNIDYNIPFT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                Best Local Similarity 100 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell cycle inhibitor
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scFv(225) (AAW05133) comprises the single-chain binding region of murine monoclonal antibody 225, which is specific for the human epidermal growth factor receptor. It is encoded by plasmid pWW152-225 (see also AAT42033), constructed by cloning MAD 225 WH and VL region cDNAs into plasmid pWW152. Novel bivalent proteins (see also AAW05134-44), some of them including scFv(225) and an effector e.g. cytotoxin, can be produced in bacterial host cells, and are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bivalent fusion proteins that bind epidermal growth factor receptor analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 88; DB 2; Length 240;
llarity 100.0%; Pred. No. 5.9e-06;
Conservative 0; Mismatches 0; Indels
                                                                                 Single chain antibody; scFv; monoclonal antibody; MAb; epidermal growth factor; receptor; antitumour; cancer;
                                                                                                                                                                                                                  1. .119

/label= VH region

/note= "monoclonal antibody 225 VH"

120. .13

/label= Linker

/note= "synthetic spacer peptide"

/label= VL
                                                                                                                                                                                                                                                                                                                                                /note= "monoclonal antibody 225 VL"
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                  Single chain antibody scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651
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ID AAW05135 standard; protein; 65

XA AAW05135;

XX

DT 29-JAN-1997 (first entry)

XX

DE scFv(225)-ETA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scFv(225)-ETA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-478748/48.
N-PSDB; AAT42033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 240 AA;
                 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1996.
                                                                                                                               Mus; sp.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wels W,
                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                 Key
Region
                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the heavy chain variable region of the murine monoclonal antibody (MAb) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stages prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                         Heavy chain, murine, mouse, monoclonal, antibody, M225, human, epidermal growth factor, EGF, receptor, inhibition, growth, tumour, cell, late stage; prostatic, prostate, variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - used
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-EGF receptor antibody 225 of late stage prostatic tumour.
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0
          100.0%; Score 88; DB 2; Length 138; larity 100.0%; Pred. No. 3.2e-06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88; DB 2; L
Pred. No. 3.2e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                         Heavy chain variable region of M225 antibody.
                                                                                                                                                                                        AAW08942 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example IV; Fig 14; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric and humanised versions of for inhibiting tumour growth, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
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100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00482982.
95US-00573289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US009847.
                                                                            15
                                                                                               69 VIWSGGNTDYNTPFT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
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                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                         1 VIWSGGNTDYNTPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 VIWSGGNIDYNTPFT
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT49340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996;
      Query Match
Best Local Simil
Matches 15; (
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                         27-AUG-2003
18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-1996,
                                                                                                                                                                                                                         AAW08942;
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                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
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AAW05133
ID AAW05
XX
AC AAW05
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Gaps

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scFv(225)-ETA (AAW05135) comprises the single-chain binding region (see also AAW05133) of murine monoclonal antibody 225, which is specific for human epidedrmal growth factor receptor, joined to exotoxin A (ETA). It is encoded by plasmid psw202-225 (see also AAT42035) obtd. by ligating an scFv(225) gene (AAT42033) into plasmid psw200 contg. the Pseudomonas acruginosa PAK ETA gene. The construct can be used to produce novel bivalent fusion proteins (see also AAW05136-44) in bacterial host cells, for use as antitumour agents
Single chain antibody; scFv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; plasmid pSW202-225; cancer; therapy; antitumour; exotoxin A; ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                             72. .38

/label= Spacer

39. .278

279. .289

/label= Scrv(225)

290. .651

/label= ETA

/note= "exotoxin A amino acids 252-613"
                                                                                                                                       . .21
/label= Sig_peptide
/note= "OmpA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 19-20; 52pp; English
                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schmidt M, Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                   95EP-00106275.
                                                                                                                                                                                                                                                                                                                                                                        95EP-00106275.
                                                          Mus sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-478748/48.
N-PSDB; AAT42035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 651 AA;
                                                                                                                                                                                                                                                                                                                                                                           26-APR-1995;
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                                                                                                                                                                                                                                                                                                                      EP739984-A1.
                                                                                                                                                                                                                                                                                                                                                30-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wels W,
                                                                                                                                        Peptide
                                                                                                                                                                                   Peptide
                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                       Peptide
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Gaps ..

Search completed: October 6, 2004, 16:29:43 Job time: 76.7895 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 16:23:59 ; Search time 15.7895 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-4 88 Title: Perfect score:

1 VIWSGGNTDYNTPFT 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	eavy	chain V	chain pr	heavy chain V r	eavy	eavy	mu chain precur		Ž	avy cha	ma-	nma-1 chain	wy chain V	wy chain V	wy chain V	wy chain V	wy cha	wy chain pr	dehydrogena	dehydrogena	chain V	chain V	in V	chain V	chain V	chain	chain V	in v	eavy chain V
	Desc		Igi	Ig h	I BI	Ig h	Ig h	II BI	anti	I pI	Ig h	DI DI	DI DI	i pi	Ig h	n pi	I P h	Ig hea	T DI	NADH	NADE	þ	б	Б	σ	Б	Ig h	מ	מ	Ig h
SUMMERTES	·	126	142	913	170	107	310	332	98	360	307	913	238	121	906	.31	128	:63	156	950	:41	105	06	22	68	92	93	125	60	86
מ	ΩĦ	PH10	A490	A259	S264	S111	GIMS	A339	PL01	D305	B318	8319	S142	8263	S145	8331	8550	838563	A324	8269	T142	S176	S144	8263	S144	S144	S144	PH10	S111	8110
	ВВ	!																0												
	Length	• н	90	100	115	115	116	116	116	121	127	135	140	114	107	121	140	117	139	337	653	95	100	106	106	107	107	109	109	112
ф	Query	6.	щ	ω.	ë.	'n.	щ.	ω.	m	щ Н	m.	'n	۳,	'n.	œ.	œ.	œ.	67.0	'n.	Η.	Η.	ö	ö			ö	ö	ö	ö	
	Score		65	65	65	92	65	65	65	65	65	65	65	64	9	9	9	59	58	54	54	53	53	53	53	53	53	53	23	53
	Result No.		7	m	4	'n	9	7	ω	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

Ig heavy chain V r	arginase - Deinoco														
811100	S11108	S11101	S11099	S11104	S11106	S11105	S11103	S11102	S10111	PL0087	A49049	S52446	H75493	S14491	PH1024
7	Ŋ	ď	~	~	7	7	N	~1	7	N	0	~1	N	(7)	0
112	112	113	114	114	114	114	115	116	117	120	122	141	301	107	110
60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	59.1	59.1
53	53	23	23	23	. 53	53	23	23	23	53	23	53	23	25	25
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

RESULT 1
PH1026
Ig heavy chain V region (clone 163-c3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C,Accession: PH1026
R,Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A, Title: Both 19M and 19G anti-DNA antibodies are the products of clonally selective B (
A; Reference number: PH0971; MUID:92381444; PMID:1512540
A, Accession: PH1026
A;Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A;Residues: 1-109 <til></til>
A;Experimental source: B cell, strain [NZB x NZW]F1
C; Superfamily: immunoqlobulin V region; immunoqlobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <imm></imm>
Query Match 76.1%; Score 67; DB 2; Length 109;
Best Local Similarity 78.6%; Pred. No. 0.0018; Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
TALINATION TO THE TA

1 VIWSGGNTDYNTPF 14 :||||||||| 50 MIWSGGNTDYNAAF 63

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Agyotz, Agyotz

Gaps ö Query Match 73.9%; Score 65; DB 2; Length 90; Best Local Similarity 78.6%; Pred. No. 0.003; Matches 11; Conservative 1; Mismatches 2; Indels

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Ig heavy chain precursor V region (MC101) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A02096
R;Kataoka, T.; Nikaido, T.; Miyata, T.; Moriwaki, K.; Honjo, T.
A;Title: The nucleotide sequences of rearranged and germline immunoglobulin V-H genes of A;Reference number: A02096; MUID:82075900; PMID:6273429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R;Daccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Broc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Itle: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-lå A;Reference number: A33932; MUID:89282823; PMID:2499887
A;Accession: A33932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 23-May-1997
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;F:1-19/Domain: signal sequence #status predicted <SIG>
F;10-116/Product: Ig heavy chain V region (MC101) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A02026.
A;Molecule type: DNA
A;Residues: 1-116 <KAT>
A;Cross_references: GB:J00502; NID:g196070; PIDN:AAA38515.1; PID:g196071
A;Note: the sequence was determined from the germine gene
                                                                                                          ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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A;Residues: 1-116 <BAC.
A;Cross-references: GB:M27107
A;Note: the authors translated the codon CTA for residue 18 as 'Csuperfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin Pregion; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.9%; Score 65; DB 2; Length 116; 78.6%; Pred. No. 0.0039; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 1; Length 116;
Pred. No. 0.0039;
1; Mismatches 2; Indels
                                                     Length 115
                                               Score 65, DB 2;
Pred. No. 0.0038;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Scor. 78.6%; Pred. No. v...
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F;15-97/Domain: immunoglobulin homology <IMM>
                                                  Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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511107
19 heavy chain V region (clone NQ2-45.10.4) - mouse (fragment)
c; pheavy chain V region (clone NQ2-45.10.4) - mouse (fragment)
c; pheavy chain V region (clone NQ2-45.10.4) - mouse (fragment)
c; phear-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
c; Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
c; Accession: M: Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A; Pritle: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A; Pritle: mRNA sequences and an unusually restricted IgG response to 2-phenyloxazolone
A; Accession: 51107
A; Status: preliminary
A; Ascession: mRNA
A; Residues: 1-115 < kAA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                        Filawler, A.M.; Lin, P.S.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987

A.Title: Adult B-call repertoire is biased toward two heavy-chain variable-region genes
A.Feference number: A94148; MUD:87175692; PMID:3104915
A.Accession: A25913
A.Accession: A25913
A.Molecule type: DNA
A.Residues: 1-100 *LAW>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology < IMM>
F:19-100/Domain: immunoglobulin homology < IMM>
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S26470
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S26470
R;Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A;Reference number: S26470
A;Reference number: S26470
                                                                                                                                                                   A25913
Ig heavy chain precursor V region (BFL2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jan-2000
C/Accession: A25913
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Pred. No. 0.0033;
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                                      43 VIWSGGSTDYNAAF 56
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Best Local Similarity 78.6
Matches 11; Conservative
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Matches 11; Conservative
     VIWSGGNTDYNTPF
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A;Molecule type: mRNA
A;Residues: 1-115 <KAV>
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à g immunoglobulin homology

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C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
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les 11; Conserv
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Matches
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130560

130 heavy chain V region (36.1.2D) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999

C;Accession: D30560

R;Matcassion: T:, Robat, E.A.

J:Immunol. 142, 863-870, 1989

A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclo
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 23-May-1997
C;Accession: B31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatth A;Taub, R.; Gould, R.J.; Hassion: B31807
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a seque A;Accession: B31807
A;Accession: B31807
A;Accession: B31807
A;Accession: preliminary
A;Accession: preliminary
A;Accession: L127 cTAU>
                                                                                                                                                     C,Accession: PL0198
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463.470, 1990
A;Fite: Variable region primary structures of monoclonal anti-DNA autoantibodies from A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0198
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                             anti-DNA autoantibody BV16-13, heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
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A)Residues: 1-121 cMAT>
A)Cross-references: GB:M24271; NID:g195617; PIDN:AAA38372.1; PID:g195618
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A) Residues: 1-116 (SMI)
A) Cross-references: GB:X53638, NID:G50191; PIDN:CAA37689.1; PID:g930137
C) Superfamily: immunoglobulin V region; immunoglobulin homology cross-references: GB:X53638, NID:G5019; immunoglobulin homology cross-references: GB:X5375, G
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Pred. No. 0.0039;
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A;Accession: D30560
A;Status: preliminary
A;Molecule type: mRNA
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78.6%;
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Best Local Similarity 'o...
-hos 11; Conservative
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Ig gamma-1 chain precursor (15C5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 614238
C;Accession: 614238
C;Accession: A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
A;Title: Construction and characterization of a recombinant murine monoclonal antibody d A;Reference number: $14236; MUID:91006173; PMID:2209622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S31913

R; Bespalov, I.A.; Hiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov submitted to the EMBL Data Library, January 1993
A; Reference number: S31913
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C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
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A;Residues: 1-140 «VAN»
A;Residues: 1-140 «VAN»
A;Cross-references: EMBL:X56392; NID:g51619; PIDN:CAA39803.1; PID:g747853
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;26-108/Domain: immunoglobulin homology «IMM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Accession: 331933
A/Molecule type: mRNA
A/Residues: 1-135 <-BES.
A/Re
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                                                       Length 127
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73.9%; Score 65; DB 2; Length 127
78.6%; Pred. No. 0.0043; 2; Indels
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78.6%; Pred. No. 0.0046; 2; Indels
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78.6%; Pred. No. 0.0047;
iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (fragment)
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Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig. gamma-2A chain precursor - mouse
                                                                                                                                                                                                                                                                1 VIWSGGNIDYNIPF 14
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33131
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 "#text_change 23-Mar-2001
C;Accession: 83131
C;Accession: 83131
A;Pescription: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jul-2000
C;Accession: S26231
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Areference number: S26309; MUID:91341421; PMID:1908510
A;Areference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S2631
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-114 «STA»
A;Cross-references: EMBL:X59176; NID:g52051; PIDN:CAA41886.1; PID:g4379205
C;Superffamily: immunoglobulin V region; immunoglobulin homology
C;Superffamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S14506
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBI. Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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A, Residues: 1-121 < TEM>
A, Cross-references: EMBL:222669; NID:g297471; PIDN:CAA80378.1; PID:g297472
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: hererotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
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A;Molecule type: mRNA
A;Residues: 1-107 <CHE.
A;Cross-references: EMBL:X58651; NID:g51291; PIDN:CAA41508.1; PID:g51292
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                     Length 114;
                                                                                                                                                                                                                                                                                                                                                                Score 64, DB 2; Length 114 Pred. No. 0.0055; 0; Mismatches 3; Indels
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Pred. No. 0.022;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.2%;
illarity 71.4%;
Conservative
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Best Local Similarity 78.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 VIWSGGTTDYNAAF 59
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Best Local Similarity
Matches 10; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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S14506
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Search completed: October 6, 2004, 16:34:46 Job time : 16.7895 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 16:21:13 ; Search time 9.21053 Seconds (without alignments) 84.800 Million cell updates/sec Run on:

US-09-635-974A-4 88 1 VIWSGGNTDYNTPFT 15 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

scriptio	P01821 mus musculu	()	P20679 podospora a		P53301 saccharomyc		mus m	ratt	뎚	P01819 mus musculu		P26023 drosophila		rattus n	xenobna	xenopus	хелор		P78540 homo sapien			P30759 xenopus lae	neuro	P18507 homo sapien	bos t	rhizopus	ovie	Q96qk1 homo sapien	mus	sarc	076324 drosophila	24 homo sap	22897
QI	HV45 MOUSE		NUSM PODAN	NUSM EMENI	YG46 YEAST	ARGI_HUMAN	ARGI MOUSE	ARGI_RAT	HV44 MOUSE	HV43_MOUSE	NUSM_NEUCR	PIG1_DROME	ARG2 MOUSE	ARG2_RAT	ARG1_XENLA	ARG2_XENLA	ARG3_XENLA	ARG1_RANCA	ARG2 HUMAN	CDGT BACOH	HIS4_BIFLO	ARGI_XENLA	ARGI_NEUCR	GAC2_HUMAN	GAC2_BOVIN	NU5M_RHIST	NPT2_SHEEP	VP35_HUMAN	VP35 MOUSE		٦,	- 1	MANR_HUMAN
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Result No.	п	N	m	4	w	G	۲	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	78	29	30	31	32	33

P43663 salmonella P31746 bacillus so	-	O9ijaz arabidopsis O9jzus neisseria m	Q9juv9 neisseria m Q01511 chlorella v		002008 photobacter P13504 mus musculu
LPFD_SALTY CDGT_BACS2	YNJ1_YEAST COAD_WIGBR	Y895 NEIMB	MICI CHVN1	AROB_STRR6	RIBB_PHOLE IL1R_MOUSE
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359	1240	220 220 220 220 220	260	355	364 576
44.9 44.9	44. 0.44.	4 4 4 4 4 4 5 6 6	4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4	44.4	44.3 44.3
39.5 39.5	39.0 30.0	ው ው ር	n m c	უ თ თ თ	თ თ ო ო
3.4 3.5	37	ж о о ч о ч	4 4 4 0 11 C	4 4 4 6	4. 4. 5.

ALIGNMENTS

RESULT 1

HV45	MOUSE
ΠD	HV45_MOUSE STANDARD; PRT; 116 AA.
AC.	,
L L	(Rel. 01, Creat
E I	(Rel. 01, Last
L I	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V region MC101 precursor.
SO	
o l	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ö	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ŏ	NCBI_TaxID=10090;
Z.	
RР	SEQUENCE FROM N.A.
X	MEDLINE=82075900; PubMed=6273429;
æ	Kataoka T., Nikaido T., Miyata T., Moriwaki K., Honjo T.;
RT	"The nucleotide sequences of rearranged and germline immunoglobulin
RT	
RT	BOUSE.
RL	J. Biol. Chem. 257:277-285(1982).
ပ္ပ	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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ر ا ا	This SWISS-DROW antry is converient It is produced through a collaboration
) E	this office the Children to Copyright Great the produced thiology a Collaboration
3 8	between the swise institute of bloming and the babb outside in
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S.C.	EMB1: JOSO2: AAA38515 1: -
6	DID. 500006. GIMETO
4 6	111 301000 GINETO
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DR	IPR007110;
DR.	InterPro; IPR003596; Ig.v.
DR	Pfam; PF00047; iq; 1.
DR.	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
¥	Immunoglobulin V reafon; Signal.
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Ę-	20 116
ı [-	N 2017 ALL OC N
1 E	011
Ξ,	116 116
SO	SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;
Ö	Oberv Match 73.9%: Score 65: DB 1: Length 116:
Be	cal Similarity 78.6%; Pred. No. 0.0022;
Ma	Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
8	1 VIWSGONTDYNTPF 14
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RESULT 2 NUSM_TRIRU

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Local Similarity 53.3 es 8; Conservative
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                                                                                                       SEQUENCE FROM N.A.
                                                             NCBI TaxID=5145;
                                                                                                                                                                                                                                                                                                         COMPLETE GENOME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de Blevre C., Dujon B.;
"Mitochondrial DNA sequence analysis of the cytochrome oxidase
"Mitochondrial DNA sequence analysis of the cytochrome oxidase
subunit I and II genes, the ArPase9 gene, the NADH dehydrogenase ND4L
and ND5 gene complex, and the glutaminy1, methiony1 and arginy1 tRNA
genes from Trichophyton rubrum.";
genes from Trichophyton rubrum.";
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                             de Bievre C., Dujon B.;
"Organisation of the mitochondrial genome of Trichophyton rubrum III.
DNA sequence analysis of the NADH dehydrogenase subunits 1, 2, 3, 4,
5 and the cytochrome b gene.";
Curr. Genet. 35:30-35(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.4%; Score 54; DB 1; Length 653; 60.0%; Pred. No. 0.7; 3; Indels iive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001750; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
Pfam; PF00662; oxidored q1; 1.
PfamTs; PF00434; NAIdored q1, 1.
PRINTS; PR0434; NADPHGRAES.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 653 AA; 73456 MW; 58207B990F568E14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-UUL-1993 (Rel. 26, Last annotation update)
NADH-ubbiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                  Q01561; Q9T9N1;
01-UUN-1994 (Rel. 29, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
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  653 AA
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EMBL, X65223; CAA46329.1; -.
PIR, 52650; S2650.
InterPro; IPR003916; NADHub_oxred5.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=IP 1817.89;
MEDLINE=99146870; PubMed=10022946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 1-337 FROM N.A.
STRAIN=IP 1817.89;
MEDLINE=92405249; PubMed=1326416;
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nes 9, Conservative
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  STANDARD;
                                                                                                                                                         Trichophyton rubrum.
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                                                                                                                                                                                                                                                                   NCBI_TaxID=5551;
                                                                                                                                                                              Mitochondrion.
                                                                                                                                 OR NADHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUSM PODAN
P20679;
  TRIRU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90291512; PubMed=2357736;
Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
"The complete DNA sequence of the mitochondrial genome of Podospora
                                                                                                                                                                                                                                                                                                 complex
                                                                                                                                                                                   STRAIN=s, and A;
MEDLINE=90204555; PubMed=2319602;
Cummings D.J., Michel F., Domenico J.M., McNally K.L.;
Cummings D.J., Michel F., Domenico J.M., McNally K.L.;
iDNA sequence analysis of the mitochondrial ND4L-ND5 gene complex
from Podospora anserina. Duplication of the ND4L gene within its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=YA2 / PYROA4 / CXXC3;
MEDLINE=89296483; PubMed=2662141;
Brown T.A., Constable A., Ray J.A., Waring R.B., Scazzocchio C., Davies R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.0%; Score 51, DB 1; Length 652; 53.3%; Pred. No. 2.1; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase, NAD, Ubiquinone, Mitochondrion.
SEOUENCE 652 AA; 72632 MW; 84CA887B75755FE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUSM EMENI STANDARD; PRT; 657 AA.
P11628; Q00181;
P10-0CT-1989 (Rel. 12, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X55026; CAA38798.1; -
PTR; 509133; S09133.
InterPro; IPR003918; NADHub_oxred4.
InterPro; IPR003916; NADHub_oxred5.
InterPro; IPR001796; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
Pfam; PF00361; oxidored_q1.
Pfam; PF00625; Oxidored_q1.1.
PRINTS; PR01434; NADBDHGNASES.
PRINTS; PR01437; NUOXDRDHASE4.
                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Hiol. 212:269-286(1990).
[2]
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Query Match
Best Local Similarity
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                                                                                                                                                                                                        SEQUENCE
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P05089;
                                                                                                                                        DOMAIN
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    RARARARARETETER
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
"Nucleotide sequence of the Aspergillus nidulans mitochondrial gene for subunit 5 of NADH dehydrogenase."; Nucleic Acids Res. 17:4371-4371(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm of Saccharomyces cerevisiae chromosome VII.",
Yeast 13.357-163(1997) TO YEAST UTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288C;
MEDILINE=97279231; PubMed=9133739;
Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
Nombela C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                           Luo X., Khanh N.Q., Wientjes F.J.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
-!- CATALVTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.8 kDa protein in BUBI-HIP1 intergenic region.
YGR189C OR G7553.
                                                                                                                                                                                                                                      EMBL; X15011; CAA33116.1; -.
EMBL; X6299; CAA4727.1; -.
PIR; S04724; S04724
InterPro; IRR00316; NADHub oxred5.
InterPro; IRR001750; Oxidored_q1.
InterPro; IRR001750; Oxidored_q1.
InterPro; IRR00150; Oxidored_q1.
Pfam; PF00361; Oxidored_q1; 1.
Pfam; PF00362; Oxidored_q1; 1.
PRINTS; PR01434; NADHDHGNASSE.
Oxidoreductaes; NAD; Ubiquinone; Mitochondrion.
SEQUENCE. 657 AA; 73361 MW; B5BB679A151E7287 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      58.0%; Score 51; DB 1; Length 657; 57.1%; Pred. No. 2.1; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                     SEQUENCE OF 316-349 FROM N.A.
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                                                                  STRAIN-NRRL 322;
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P53301;
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Matches
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TISSUE=Liver;
MEDLINE=22380257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Ditchendo L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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"Human liver-type arginase gene: structure of the gene and analysis
of the promoter region."
Nucleic Acids Res. 16:8789-8802(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and nucleotide sequence of cDNA for human liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haraguchi Y., Takiguchi M., Amaya Y., Kawamoto S., Matsuda I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50.5; DB 1; Length 507;
Pred. No. 1.9;
2; Mismatches 2; Indels 1
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-SER.
7D7B61F57AEA942C CRC64;
PIR; S64507; S64507.

HSSP; P23304; JAJK.
Germonine; 141501; ---
SGD; S0003421; CRH1.
GO; G0:0009277; C:cell wall (sensu Fungi); IDA.
GO; G0:0000131; C:incipient bud site; IDA.
InterPro; IPR00898; ConAlike lec gl.
InterPro; IPR00757; Glyco.hydro_16.
Pfan; PF00722; Glyco.hydro_16; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arginase.";
Proc. Natl. Acad. Sci. U.S.A. 84:412-415(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)
                                                                                                                                                                                                                                                                                                                                           POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                            POLY-SER
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345 357 POO
387 391 POO
467 470 POO
507 AA; 52757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%;
64.3%;
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Farben D.K., Esteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schuutz S.Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences., Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATALITICATION OF STATE ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.
-!- CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.
-!- COPACTOR: Manganese.
-!- PATHWAY: Arginine degradation via the urea cycle; first step.
-!- SUBUNIT: Homotrimer.
-!- SUBUNIT: Homotrimer.
-!- INDUCTION: By arginine or homoarginine.
-!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                   Uchino T., Haraguchi Y., Aparicio J.M., Mizutani N., Higashikawa M., Naitoh H., Mori M., Matsuda I.;
"Three novel mutations in the liver-type arginase gene in three unrelated Japanese patients with argininemia.";
Am. J. Hum. Genet. 51:1406-1412(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95377725; PubMed=7649538;
Orbino T., Snyderman S.E., Lambert M., Qureshi I.A., Shapira S.K.,
Sansaricq C., Smit L.M.E., Jakobs C., Matsuda I.;
"Molecular basis of phenotypic variation in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT SER-290.
MEDLINE=92286280; PubMed=1598908;
Grody W.W., Xlein D., Dodson A.E., Kern R.M., Wissmann P.B.,
Goodman B.K., Bassand P., Marescau B., Kang S.-S., Leonard J.V.,
Cederbaum S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular genetic study of human arginase deficiency."; Am. J. Hum. Genet. 50:1281-1290(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 207800; -.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004053; F:arginase activity; TAS.
GO; GO:0006527; P:arginine catabolism; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS ARGININEMIA THR-11 AND VAL-138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X12662, CAA31188.1;

EMBL, X12663, CAA31188.1;

EMBL, X12664, CAA31188.1;

EMBL, X12664, CAA31188.1;

EMBL, X12665, CAA31188.1;

EMBL, X12666, CAA31188.1;

EMBL, X12667, CAA31188.1;

EMBL, X12669, CAA31188.1;

EMBL, X12669, CAA31188.1;

EMBL, A121275, CAB3128.1;

EMBL, BC020653; AAH20653.1;

ESPP, P07824, 3R.A.

GK, P05089; ---

MIM, 207800; ---
                                                                                                                                                                                                                                                     VARIANT ARGININBMIA ARG-235.
MEDLINE=93098256; PubMed=1463019;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERAIN-FYB/N; TISSUE-Liver, and Mammary gland;

MEDLINE-22388257; Pubmed=1247932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A piacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A piacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong D.,

Brownstein M.J. Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malk J.A., Gibbs R.A.,

Richards S., Morley K.C., Halte S., Garcia A.M., Gay L.J., Hulyk S.W.,

Kallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miltalow M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                        MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
I -> T (in argininemia; 12% of wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                           / FTId=VAR_015595.

G -> W (in argininemia).

G -> R (in argininemia).

FTId=VAR_000674.

T -> S (could be a polymorphism).

/FTId=VAR_000675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chieko H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                     PROSITE; PS00148; ARGINASE_2; 1.
PROSITE; PS01053; ARGINASE_3; 1.
Urea cycle; Arginine metabolism; Hydrolase; Manganese;
Disease mutation; Polymorphism.
METAL 101 MANGANESE 1 (BY SIMILARIT)
                                                                                                                                                                                                                                                                                                                                                                                                                                    -> Q (IN REF. 1).
8F3BE2652243F622 CRC64;
                                                                                                                                                                                                                                                                                                                 /FTId=VAR 015594.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA
                                                                                                                                                                                                                                                                                                  activity)
InterPro; IPR006035; Arg agm_form.
InterPro; IPR005924; Arginase.
Pfam; PF00491; arginase; 1.
FIGREAMS; PR00111, ARGINASE.
FIGREAMS; TIGR01229; rocF arginase;
PROSITE; PS00147; ARGINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                        290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Q61176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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METAL
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D.W.;

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                                                                                   MEDLINE=87194847; PubMed=3571256; Kavamoro S., Amaya Y., Murakami K., Tokunaga F., Iwanaga S., Kobayashi K., Saheki T., Kimura S., Mori M.; "Complete nucleotide sequence of cDNA and deduced amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

X O'D., Kim N.N., Traish A.M., Christianson D.W.;

A COX J.D., Kim N.N., Traish A.M., Christianson D.W.;

A Cox J.D., Kim N.N., Traish A.M., Christianson D.W.;

T erectile function.";

I Nat. Struct. Biol. 6:1043-1047(1999).

I Nat. Struct. Biol. 6:1043-1047(1999).

- CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.

- CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.

- SUBUNIT: Homographer.

- SUBUNIT: Homographer.

- SUBUNIT: BOCATION: Cytoplasmic.

- SUBULILLAR LOCATION: Cytoplasmic.

- INDUCTION: By arginine or homographine.

- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                     MEDLINE=97002331; PubMed=8849731; Ash D.B., Christianson D.W.; Ash D.B., Christianson D.W.; Structure of a unique binuclear manganese cluster in arginase."; Nature 383:554-557(1996).
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97410344; PubMed=9265637; Scolnick L.R., Kanyo Z.F., Cavalli R.C., Ash D.E., Christianson D "Altering the binuclear manganese cluster of arginase diminishes thermostability and catalytic function."; Biochemistry 36:10558-10565(1997).
                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO0116; ARGINASE.
TIGREAMS, TIGR01229; rocF arginase,
PROSITE, PS00147; ARGINASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; MI7931; AAA40760.1; --
EMBL; MI7924; AAA40760.1; --
EMBL; MI7926; AAA40760.1; JOINED.
EMBL; MI7926; AAA40760.1; JOINED.
EMBL; MI7926; AAA40760.1; JOINED.
EMBL; MI7929; AAA40760.1; JOINED.
EMBL; MI7929; AAA40760.1; JOINED.
EMBL; MI7920; AAA40760.1; JOINED.
EMBL; MI7920; AAA40760.1; JOINED.
EMBL; MI7920; AAA40760.1; JOINED.
EMBL; JO
                                                                                                                                                                        rat liver arginase.";
Biol. Chem. 262:6280-6283(1987)
      Chem. 263:2245-2249(1988)
                                                SEQUENCE FROM N.A.
        Biol.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Liver:

#BDLINE-88115364; PubMed-2892837;
Ohtake A., Takiguchi M., Shigeto Y., Amaya Y., Kawamoto S., Mori M.;

Structural organization of the gene for rat liver-type arginase.";
                                                                                                                                                                                                                                                                                                                                                                                                              Redriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; perc. hall 15,000 full-length human and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-ornithine + urea. COFACTOR: Manganese.
-!- PATHWAY: Arginine degradation via the urea cycle; first step..-!- SUBUCELLULAR LOCATION: Cytoplasmic.'
-!- SUBCELLULAR LOCATION: Cytoplasmic.'
-!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Pred. No. 1.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1988 (Rel. 08, Created)
01-ARF-1990 (Rel. 14, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34808 MW;
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Local Similarity 60.0%;
nes 9; Conservative 1
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126
128
128
232
234
234
323 AA)
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P07824;
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SEQUENCE
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Matches
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                                                                                                                           MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation
"Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MANDERS, MEDITINE-8101213; PubMed=6774258; MADLINE-8101213; PubMed=6774258; Maxi R., Kurosawa Y., Roeder W., Tonegawa S.; Two types of somatic recombination are necessary for the generation "Two types of somatic recombination are necessary for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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1-JUL 1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 141 precursor.
1g heavy chain V region C 141 precursor.
Eukaryota; Metazoa (Pordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 1.4;
3; Mismatches 2; Indels
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IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 286:676-683 (1980):
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERM: PF00047; 1g; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                      10-OCT-2003 (Rel. 42, Last annotation update) Ig heavy chain V region PJ14 precursor. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                      PIR, A02095; HVMS14.
PDB; LANN; 29-APR-98.
PDB; LANO; 29-APR-98.
PDB; LANP; 29-APR-98.
PDB; LANP; 29-APR-98.
PDB; LANP; 29-APR-98.
PDB; LG7H; 17-JAN-01.
PDB; LG7H; 17-JAN-01.
PDB; LG7M; 17-JAN-01.
PDB; LG7M; 17-JAN-01.
PDB; A3C9; 24-JUL-02.
PDB; A3CA; 24-JUL-02.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%;
                                                                                                                                                                                                                                                                                                                              EMBL; V00767; CAA24148.1; -.
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115 AA;
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Best Local Similarity
7, Conserv
                                                                                                                 SEQUENCE FROM N.A.
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P01819;
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NON TER
SEQUENCE
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PROSITE; PS00148; ARGINASE 2; 1.
PROSITE; PS01053; ARGINASE 3; 1.
Urea cycle; Arginine metabolism; Hydrolase; Manganese; 3D-structure.
METAL 101 MANGANESE 1.
METAL 124 MANGANESE 2.
METAL 128 128 MANGANESE 2.
METAL 128 232 MANGANESE 1.
METAL 232 232 MANGANESE 1.
METAL 232 232 MANGANESE 1.
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Pred. No. 1.4;
1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.8%;
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Best Local Similarity 60.0
Matches 9, Conservative
                                                                                                                                                          164
169
173
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193
199
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323 AA;
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TURN
SEQUENCE
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HELIX
TURN
STRAND
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HV44 MOUSE
ID HV44 MC
AC P01820;
DT 21-JUL-
DT 21-JUL-
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Query Match
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PIG1 DROME
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. The Buropean Boinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980).
-!- MISCELLANDOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A WYELOMA THAT SECRETES IGG2B.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=St. Lawrence 74 / St 74 / ORS 6A;
MEDLINE=87228330; PubMed=3035337;
Melson M.A., Macino G.;
Structure and expression of the overlapping ND4L and ND5 genes of Neurospora crassa mitochondria.";
Mol. Gen. Genet. 206.307-317(1987).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.

Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION MOPC 141.
IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.4%; Score 47; DB 1; Length 144; 63.6%; Pred. No. 1.8; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-REB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X05115, CAB37187.1; -. PIR; S10843; S10843. InterPro, IPR003918; NADHub_oxred4
                                                                                                                                                                                                                          EMEL, V00768; CAA21149.1; --
PIR, A02094; G2MS14.
HASP; POURSE; 7FAB.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig-v.
Pfan; PF00047; ig; 1.
PMART; SM00406; Igv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 IWGNGSTDYNS 80
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P05510;
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SEQUENCE
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NUSM_NEUCR
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MEDLINE=20196006; PubMed=10731132;

XR MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Adams M.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

A burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Upstream sequences of dosage-compensated and non-compensated alleles of the larval secretion protein gene Sgs-4 in Drosophila."; Chromosoma 96:1-7(1987).
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Canton-S;
MEDLINE=92120020; PubMed=1769273;
Furia M., Digllio F.A., Artiaco D., D'Avino P.P., Cavaliere D.,
Folito L.C., "Molecular organization of the Drosophila melanogaster Pig-1 gene.";
Chromosoma 101:49-54(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIGI_DROME STANDARD,
PIGI_DROME STANDARD,
P26023; 076914; 024519; 0904T3;
01-MAY-1992 (Rel. 22, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
PIGI OR PIG-1 OR GSG OR EG;96G10.1 OR CG10790.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Braryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CDL TaxID=7227;
                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                Score 46; DB 1; Length 715; Pred. No. 14; 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Oregon-R;
Bolshakov V., Borkova D., Minana B., Kafatos F.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR003916; NADHub_oxred5.
InterPro; IPR001756; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
Pfam; PF00561; oxidored q1; 1.
Pfam; PF00562; oxidored q1; 1.
PRINTS; PR01434; NADHDFGNASE5.
PRINTS; PR01437; NUOXDRDTASE4.
Oxidoreductase; NAD; UDiquinone; Mitochondrion.
SEQUENCE 715 AA; 79817 MW; CFAAF0F45FAAC277 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAINS-Oregon-R, Karsnas, and Samarkand;
MEDLINE-88136816, PubMed=3125018;
Hofmann A., Korge G.;
                                                                                                                                                                                                                                     52.3%;
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185 VLWTLGNLDYATVFS 199
                                                                                                                                                                                                                                                                                                                              1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                        Local Similarity 53.3
hes 8; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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354 AA.

STANDARD;

MOUSE

Thu Oct 14 09:36:58 2004

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Glodek A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Henris M., Houston K.A., Howland T.J., Hermandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., MoPherson D., Mont S.M., Moy M., Murphy B., McDherson D., Moshrei B., McIntosh T.C., McLeod M.P., Moshrefi A., Nelson C.M., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Nelson D.R., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parle D.L., Shue B.C., Siden-Kiamos G.S., Pan S., Pollard J., Puri V., Reese M.G., Shue B.C., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Shue B.C., Stapleton M., Skupski M.P., Smith T., Shies R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstcok G.M., Weissenbach J., Nare J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q., Zhao Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Through W., Zhou X., Zhu S., Zhu X., Smith H.O., Lenner 20195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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I -> R (IN REF. 1).

I -> T (IN REF. 3).

NUNKKTANSNNHRRRAGASNNHNKRRASNNNSRR

RG -> TITRRGPIATTIAKGREPTITIKRHPTITAQAQE

OOFQEAWLERKWLKQQLHVDYMHNKYFFCS (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF. 2).
KKASINNISHRRUNNISHRG -> RRHPTTTTGAGTTIPGG
KKASINNISHRRUNNISHRG (IN REF. 1 AND 2).
4 DEB6346D6713841 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRE-INTERMOULT GENE-1 PROTEIN.
ALA/ASP/THR-RICH.
ALA/ASP/TRS-RICH.
3 X G AA TANDEM REPEATS OF S-S-A-D-S-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Not known.
-!- TISSUE SPECIFICITY: Low amounts in first to third instar larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels

    -!- DEVELOPMENTAL STAGE: Throughout the larval period.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M24138; AAA28893.1; -.
EMBL; XI5760; CAA33767.1; -.
EMBL; ALO24484; CAA19669.1; -.
EMBL; AE003427; AAF45659.1; -.
Flybase; FBGN003086; Pigl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 AA; 18142 MW;
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Matches 8; Conservative
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SIGNAL 1
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REPEAT
CONFLICT
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4 SGGNTDYNTPFT 15 || :|||:|| | 83 SGSDTDYDTPTT 94

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RESULT 13 ARG2_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Arginine degradation via the urea cycle; first step. -!- SUBUNIT: Homotrimer (By similarity). -!- SUBCELLULAR LOCATION: Mitochondrial. -!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CC7BL/6J; IISSUE=Kidney;
MEDLINE=99032597; PubMed=9814991;
Morris S.M. dr., Kepka-Lenhart D., Chen L.C.;
"Differential regulation of arginases and inducible nitric oxide synchase in murine macrophage cells.";
Am. J. Physiol. 275:E740-E747(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthesis (By similarity).
CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.
COFACTOR: Manganese.
                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginase II, mitochondrial precursor (EC 3.5.3.1) (Non-hepatic arginase) (Kidney-type arginase).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Iyer R.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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PROSURE; PRO148; ARGINASE 1; 1.

PROSURE; PRO1053; ARGINASE 2; 1.

PROSURE; PRO1053; ARGINASE 3; 1.

PROSURE; PRO1053; ARGINASE 3; 1.

PROSURE; PRO1059; ARGINASE 3; 1.

PROMISE PRO1059; ARGINASE 3; 1.

PROSURE PRO1059; ARGINASE 3; 1.

PROSURE PRO1059; ARGINASE 3; 1.

PROSURE PRO1059; ARGINASE 3; 1.

PROSURE; PRO1059; ARGINASE 3; 1.

PROSURE PRO1059; ARGINASE 3; 1.

PROSURE PRO1059; ARGINASE 3; 1.

PROSURE PRO1059; ARGINASE 3; 1.

PROMISE PRO1059; ARGINASE 3; 1.

PROTUST PROTUST
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EMBL, AF032466; AAR86959.1; -...
EMBL, AF044680; AAC78460.1; -...
EMBL, AF0445969; AAC78460.1; JOINED.
EMBL, AF045969; AAC78460.1; JOINED.
EMBL, AF045961; AAC78460.1; JOINED.
EMBL, AF045964; AAC78460.1; JOINED.
EMBL, AF045964; AAC78460.1; JOINED.
HSSP, P07824; LD3V.
MGD, MGI.1330806; ARG.
INTERFED; IPR005924; ARGINASE.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Kidney;
                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Wister; TISSUE-Small intestine;

X MEDINE-9705363; PubMed=8898077;
GOTON T., Sonoki T., Nagasski A., Texada K., Takiguchi M., Mori M.;
GOTON T., Sonoki T., Nagasski A., Terada K., Takiguchi M., Mori M.;
T. darginase II) and comparison of its induction with nitric oxide
T. darginase II) and comparison of its induction with nitric oxide
Synthase in a murine macrophage-like cell line.";
FEBS Lett. 395:119-122(1996).

-!- FUNCTION: May play a role in the regulation of extra-urea cycle
arginine metabolism and also in down-regulation of nitric oxide
Synthesis (By similarity).
-!- COFACTOR: Manganese.
-!- CATAUTY: L-arginine + H(2)O = L-ornithine + urea.
-!- COFACTOR: Manganese.
-!- PATHWAY: Arginine degradation via the urea cycle; first step.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                      MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARG2_RAT STANDARD; PRT; 354 AA.
008701; P97539;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginase II, mitochondrial precursor (EC 3.5.3.1) (Non-hepatic arginase) (Kidney-type arginase)
                                                                                                                                                                                                                51.1%; Score 45; DB 1; Length 354; 53.3%; Pred. No. 9.3;
                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iyer R.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    B372DF68A19473F2 CRC64;
                                                                                                                                                                                                                                                                  Mismatches
ARGINASE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00491, arginase; 1.
PRINNES, PR00116; ARGINASE.
TIGRRAMS; TIGR0129; rocf arginase; 1.
PROSITE; PS00147; ARGINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Sprague-Dawley; TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR006035; Arg agm form
InterPro, IPR005924; Arginase.
                                                                                                                                                                  38878 MW;
                                                                                                                                                                                                                                                                                                                                                           139 VIWVDAHADINTPLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 87-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D86928; BAA13183.1; -. P07824; 1D3V.
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                                                                                                                                                                                                                                                                                                             1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                Conservative
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23
120
143
145
147
251
354 AA;
                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
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                    METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (stages
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J. Biol. Chem. 269:25328-25334(1994).
-!-PUNCITON. As well as its role in the urea cycle, may be involved in tissue remodeling.
-!-CATALYTIC ACTIVITY: L-arginine + H(2)O = L-ornithine + urea.
-!-COFACTOR: Manganese (By similarity).
-!-PATHWAY: Arginine degradation; first step.
-!-SUBINIT: Homotrimer (By similarity).
-!-TISSUE SPECIFICITY: Expressed at differing tadpole stages in tail, integrine, hindlimb and trunk region. Most abundant in tadpole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: First detected in neurula (stage 16/17). Highest levels in whole tadpole found around stage 47/48. In the lintestine, increased levels are found during metamorphosis (stage 58-64). Low levels expressed in hindlind until stage 66 after which, levels dramatically increase. In the tail, a constant high level of expression is found throughout metamorphosis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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MEDLINE=95014323; PubMed=7929226;
Patterton D., Shi Y.-B.;
"Thyroid hormone-dependent differential regulation of multiple
                                                                                                                                                                                                                                                                                                                   2 (BY SIMILARITY) SIMILARITY).
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PROSITE; PS00148; ARGINASE_2; 1.
PROSITE; PS01053; ARGINASE_3; 1.
Urea cycle; Arginine metabolism; Hydrolase; Manganese;
Transit peptide; Mitochondrion.
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                                                                                                                                                                                                                                 ARGINASE II.

MANGANESE I (BY S
MANGANESE I IN REF: 2
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Pred. No. 9.3;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginase, non-hepatic 1 (EC 3.5.1).
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NCBI_TaxID=8355;
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Les 8; Conserv
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Q91553;
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
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51.1%; Score 45; DB 1; Length 360;
Best Local Similarity 53.3%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                    EMBL, U08406; AAA56891.1; -
PIR, IS1663, I51663.
RISSP, PO7824; 1D3V.
InterPro; IPR005924; Arginase.
InterPro; IPR005924; Arginase.
PEAM; PR00116; ARGINASE.
PRINTS; PR00116; ARGINASE.
ITGREAMS; TIGRIANSE.
PROSITE; PS00147; ARGINASE.
PROSITE; PS00149; ARGINASE.
IVea cycle; Arginine metabolism; Hydrolase; Manganese;
Multigene family.
METAL 145 MANGANESE I AND 2 (BY SIMILARITY).
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253 MA
255 MA
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141 VIWVDAHADINTPLT 155 1 VIWSGGNTDYNTPFT 15 g δ

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Search completed: October 6, 2004, 16:30:24 Job time: 11.2105 secs

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October 6, 2004, 16:23:13 ; Search time 50.2632 Seconds (without alignments) 94.160 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          1017041 segs, 315518202 residues
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Maximum Match 1008
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Ogrw15 deinococcus Q91tn5 tupaia herp Q88hp7 trichoderma Q9bs50 homo sapien Q8yxd0 anabaena sp Q95jc8 sus scrofa Q8cv12 homo sapien Q80v14 mus musculu Q9hbc6 cryphonectr Q8hus cryphonectr Q8hu2 cryphonectr Q8hd2 cryphonectr Description Q9FWLS Q91TN6 Q8FB77 Q9FXD0 Q95JC8 Q8TF72 Q8TF72 Q8UV14 Q91X92 Q8HHC6 Q8HHC6 Q8HHC6 Q8HHC6 Q8HHC7 Q8HHC6 Q8HHC7 Q8HHC7 Q8HHC7 % Query Match Length DB CO C Score Result

SUMMARIES

Traction sequence of the radioresistant bacterium Deinococcus addiodurans R1.";

Science 286:1571-1577(1999).

EMBL, AE0019225, AAF10226.1;

R PIR, H75493; H75493.

R TIGR, DR0651, 2CEV.

R TIGR, DR0651, P: carginase activity; IEA.

R GO; GO:0004053; F: raginase activity; IEA.

R GO; GO:0004053; F: carginase activity; IEA.

R GO; GO:000452; F: carginase activity; IEA.

R GO; GO:000524; F: carginase.

R InterPro; IPR005924; Arginase.

R InterPro; IPR005035, Arginase.

R Pfam; PF00491; arginase. 1.

InterPro, IPR006035; Arg_agm_form.
Pfam; PF00491; arginase; 1.
Pfam; PS00116; ARGINASE.
TIGRPAMs; TIGR01229; rocF_arginase; 1.

Q97dn6 clostridium Q872j1 neurospora Q97ym6 sulfolobus

Q97DN6 Q872J1 Q97YM6

	OS6785 stathyloco O86785 stathyloco Q88452 bacteroid O42800 aspergillu Q87947 bacterioph Q95045 rhicobium Q86147 shewanell O42795 collectori Q99012 trichoderm Q9012 trichoderm Q9012 trichoderm Q9019b8 leishmania Q84612 vibrio vu Q84612 streptoco Q89hh8 bradyrhiz Q99ng4 mus muscu Q89hh8 bradyrhiz Q99ng4 mus muscu	ALIGNMENTS RT; 301 AA. ated) t sequence update) t annotation update)	Deinococcaus radiodurans. Deinococcaceae, Deinococcus-Thermus, Deinococcales, Bacteria, Deinococcus-Thermus, Deinococcaceae, Deinococcaceae, Deinococcus. NCBI_TaxID=1299, [1] SEQUENCE FROM N.A. STRAIN=R.1 / ATCC 13939 / DSM 20539 / NCIB 9279; MEDLINE=20036896, PubbMed=10567266, MEDLINE=20036896, PubbMed=10567266, Medite O., Bisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haff D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Waathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M., Genome sequence of the radioresistant bacterium Deinococcus
Q826K9 Q9RJZ8 Q97ME6 Q87ME6 Q87ME6 Q897ME6 Q897X5 Q82TQ2 Q8333 Q8333 Q8333 Q8333 Q84734	056785 QBHG56 QBHG75 QQ2MD74 QY4Q7 QY4Q7 QBE147 QBE147 QBE147 QBE147 QBON9B6 QBON9B6 QBON9B6 QBON9B6 QBON9B6 QBON9B6 QBON9B6	ALIGN PRT; Created) Last sec	icus. SM 20539 / SSM 20539 / idelberg J. F Gwinn M.L., ng L., Pamph M.Conald L., Agland L., Salzberg L., Salzberg J., M.Conald L., M.Conald L., M.Conald L., M.Conald L., M. Calzberg L., radioresista
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56.8%; Score 50; DB 4;
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TIGREAMS: TIGRO1229; rocF arginase; 1.
PROSITE; PSOO147; ARGINASE 1; 1.
SEQUENCE 236 AA; 25356 WW; 79F02C6
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01-OCT-2003
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Q9BS50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BS50
RRT RRT RR RA BRIT DR RR BRIT DR BRIT 
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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gabs
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Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
Ferreira Junior J.R., Abrahao-Neto J., Farah J.P.S., El-Dorry H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocrecmycetidae; Hypocreales; Hypocreaceae; Hypocrea.

NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                          Score 53; DB 16; Length 301;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 12; Length 575;
Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                      3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01673; Herpes env; I.
SEQUENCE 575 AA; 63743 MW; BE62BEF35166825D CRC64;
                                                                                                                                   301 AA; 32339 MW; 9DDD18F99E744682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tupaia herpesvirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 58.0%; Score 51; DB Local Similarity 57.1%; Pred. No. 8.5; es 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADH-ubiquinone oxidoreductase chain 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=2;
MEDLINE=21211637; PubMed=11312357;
    PS00147; ARGINASE_1; 1. PS00148; ARGINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virol. 75:4854-4870(2001).
                                                                                                                                                                                                                          69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 VIWVDAHTDYNTP 130
                                                                                                                                                                                        Query Match
Best Local Similarity 69.22
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              1 VIWSGGNTDYNTP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
    PROSITE; PS00147; AR PROSITE; PS00148; AR Complete proteome. SEQUENCE 301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpesvirus.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10397;
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Matches
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Q8SHP7
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091TM6
001TM0
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Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
Chambergo F.S., Bonaccorsi E.D., Ferreira J.J.S., El-Dorry H.;
Ferreira Junior J.R., Abrahao-Neto J., Farah J.P.S., El-Dorry H.;
Submitted (NOV-2001) to the EMEL/GenBank/DDBJ databases.
EMBL; AF447590; AAL74164.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0009137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
"Elucidation of the Metabolic Fate of Glucose in the Filamentous Fungus Trichoderma reesel Using Expressed Sequence Tag (EST) Analysis and cDNA Microarrays.";
J. Biol. Chem. 277:13983-13988 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skeletal muscle;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC005321, AAH05321.1, --
EMBL, BT006741, AAP35387.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003916, NADHUD. oxred5.
InterPro; IPR001750; Oxidored q1.
InterPro; IPR001750; Oxidored q1.
InterPro; IPR001361; Oxidored q1.N.
Pfam; PF00662; Oxidored q1.N.
Pfam; PF00662; Oxidored q1.N.
PRINTS; PR01434; NADHDRÄNSES.
BROUNCS; Oxidored: VDiquinone; Mitochondrion.
SEQUENCE 692 AA; 77171 MW; 89821FAAFCBA6C81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79F02C69B700AB67 CRC64;
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GO; GO:0003824; Frantalytic activity; IEA.
GO; GO:0006527; Pranginine catabolism; IEA.
Interpro; IPR005924; Arginase.
InterPro; IPR006035; Arg. agm. form.
Ffam; PF00491; arginase; 1.
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Length 236;

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Gaps

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01-JUN'2003 (TrEMBLrel. 24, Created)
01-JUN'2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arginase 1, liver.
Mans musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ANO14488; AALT1547.1.
GO; GO:0004053; F:arginase activity; IEA.
GO; GO:000527; F:arginase catabolism; IEA.
InterPro; IPR006035; Arginase.
InterPro; IPR06035; Arginase.
PRINTS; PR00116; ARGINASE.
TIGREAMS; TIGR01229; rocf_arginase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.8%; Score 50; DB 4; Length 330; 60.0%; Pred. No. 6.6; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                    Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                          Hydrolase.
SEQUENCE 322 AA; 35018 MW; D99FB071CB916B2F CRC64;
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PROSITE; PS00147; ARGINASE 1; 1.
PROSITE; PS01049; ARGINASE 2; 1.
PROSITE; PS01053; ARGINASE 3; 1.
SEQUENCE 330 AA; 35664 WW; 5747D414E8741D7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arginase type I erythroid variant.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                            Query Match 56.8%; Score 50; DB 6; Best Local Similarity 60.0%; Pred. No. 6.4; Matches 9; Conservative 1; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 AA
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                                             PRINTS; PROO116; ÅRGINASE.
TIGRRAMS; TIGRO1229; TOCF arginase; 1.
PROSITE; PSOO147; ARGINASE 1; 1.
PROSITE; PSO1048; ARGINASE 2; 1.
PROSITE; PSO1053; ARGINASE 2; 1.
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STRAIN-CZECH II, TISSUE-Breast tumor;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 VIWVDAHTDINTPLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 VIWVDAHTDINTPLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNTDYNTPFT 15
           Pfam; PF00491; arginase; 1. PRINTS; PR00116; ARGINASE.
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxiD=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Q8TE72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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                                             Gaps
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N 11,

N 11,

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N NLI,

N MEDLINE=21595285; PubMed=11759840;

N Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

N Matanabe A., Iriguchi M., Ishikawa A., Kawashima X., Kimura T.,

N Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

N Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

N Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

N Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

R. Complete genomic sequence of the filamentous nitrogen-fixing

R. Complete genomic sequence of the filamentous nitrogen filamentous nitrog
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OJUDEC-2001 (TERMELrel. 19, Created)
OJ-DEC-2001 (TERMELrel. 19, Last sequence update)
OJ-UN-2003 (TERMELrel. 24, Last annotation update)
OJ-UN-2003 (TERMELrel. 24, Last annotation update)
Sus scrofa (Pig. 3.5.3.1).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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"Sequence of Pig Arginase I.";
"Sequence of Pig Arginase I.";
"Sequence of Oun-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039112, AAR91874.1;
"GO; GO:0004053; F:arginase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0006527; P:arginine catabolism; IEA.
InterPro; IPR005924; Arginase.
InterPro; IPR005035; Arg_agm_form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 AA; 30913 MW; AE7C2E0D454E41FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                             .,
21
Best Local Similarity 60.0%; Pred, No. 4.5; Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      288 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-UTN-2003 (TrEMBLrel. 24, Last ann
Permease protein of ABC transporter.
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                  120 VIWVDAHTDINTPLT 134
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114 LIWGGRNQNYNLPIT 128
                                                                                                         1 VIWSGGNTDYNTPFT 15
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Best Local Similarity 53.3
Matches 8; Conservative
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Anabaena sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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102 ILWSLGNLDYATVFS 116
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Best Local Similarity 55...
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                        STRAIN=I-7;
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Q8HAU8
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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E Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0004053; F:arginase activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

R GO; GO:000527; P:arginase activity; IEA.

R InterPro; IPR005034; Arginase.

R InterPro; IPR005035, Arginase.

R PEAM; PR0041; arginase:1.

R PRINTS; PR00116; ARGINASE:1.

R PROSITE; PS00147; ARGINASE:1:1

R PROSITE; PS00149; ARGINASE:2:1.

R PROSITE; PS00149; ARGINASE:2:1.
                                                                                                                                                                                                                                                                                                                            Query Match 56.8%; Score 50; DB 11; Length 335; Best Local Similarity 60.0%; Pred. No. 6.7; Matches 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%; Score 49; DB 11; Length 482; 66.7%; Pred. No. 15; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryphonectria parasitica (Chesnut blight fungus) (Endothia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO11181, AAH11181.1; -
PIR, F33932; F33932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfan, PF00047; ig; 4. ——
Pfan, PF00047; ig; 4. ——
PROSITE; PS00315; IG_LIKE; 4. —
PROSITE; PS00230; IG_MHC; 2. —
Hypothetical protein—
SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MDR-2003 (TrEMBLrel. 23, Created)
01-MDR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH-ubiquinone oxireductase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 VIWVDAHTDINTPLT 146
                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPFT 15
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Q91X92;
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08HHGC
10 08HHGC
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DT 01-MAJ
DT 01-MAJ
DT 01-MAJ
DT 01-MAG
ON NDS.
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mineacures, Principal pacemponents and complex; Cryphonectria.

Or Cryphonectria. Endethia complex; Cryphonectria.

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[1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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NCBI_TaxID=1488;
  NCBI_TaxID=5116;
                                                                                                                                                                                                                                                            SEQUENCE
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Matches
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradythiczblum japonicum USDA110.";
DNA Res. 9:189-197(2020)
EMBL; AP005957; BAC51387.1; -..
EMBL; AP005957; BAC51387.1; -..
GO; GO:0004053; F:arginase activity; IEA.
GO; GO:000524; F:arginase activity; IEA.
GO; GO:000527; P:arginiase activity; IEA.
InterPro; IPR005054; Arginase.
InterPro; IPR005054; Arginase.
InterPro; IPR0050534; Arginase.
InterPro; IPR0050534; Arginase.
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Sordariomycetidae, Diaporthales, Valsaceae,
Cryphonectria-Endothia complex; Cryphonectria.
                                                                                                                                                                                                                                                                      Bradyrhizobium japonicum.
Bradyrhizobium japonicum.
Bradyrhizobiacenia; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Match 54.5%; Score 48; DB 16; Length 325;
Local Similarity 53.3%; Pred. No. 14;
les 8; Conservative 2; Mismatches 5; Indels
                        Query Match
54.5%; Score 48; DB 8; Length 136;
Best Local Similarity 53.3%; Pred. No. 5.2;
Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryphonectria parasitica (Chesnut blight fungus) (Endothia
15204 MW; F9B296B6EB99BD99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 AA; 35660 MW; 92964D631E8D2BCD CRC64;
                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                          325 AA
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01-MAR-2003 (TrEMBLrel. 23, Last sequen
01-0CT-2003 (TrEMBLrel. 25, Last annota
NADH-ubiquinone oxireductase subunit 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0147; ARGINASE 1; 1.
PROSITE; PSO0148; ARGINASE 2; 1.
PROSITE; PSO1053; ARGINASE 3; 1.
Complete proteome 325 AA; 3560 MW; 92
                                                                                           01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 VLWLDAHADYNTPET 145
                                                                             1 VIWSGGNTDYNTPFT 15
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                                                                                                                                                                          PRELIMINARY;
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136 AA;
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Mitochondrion.
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SEQUENCE
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Q89H72
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Gobbi E.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR46638; AA014099.1;

GO; GO:0008137; E:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0006120; P:Nitochondrial electron transport, NADH to u. .; IEA.

InterPro; IPR00316; NADHub_oxred4.

InterPro; IPR00176; Oxidored_q1.

InterPro; IPR001176; Oxidored_q1.

InterPro; IRR001816; Oxidored_q1.

Fam; PP00561; oxidored_q1.

PRINTS; PR01434; NADHDHGNASE4.
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XX MEDLINR=21589325; PubMed=11466286;

XM MEDLINR=21589325; PubMed=11466286;

XM Gling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

XM Glison K., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Tatusov R.L., Sabathe F., Daly M.J.,

XM Tatusov R.L
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable alpha-arabinofuranosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%; Score 48; DB 8; 53.3%; Pred. No. 30; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     835 AA.
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520 MIWFNGNTNYVTP 532
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1es 8; Conservative
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ID 087211 PRELIMINARY; PRT; 301 AA.

AC 087221; PRELIMINARY; PRT; 301 AA.

DT 01-UUN-2003 (TERMBLrel. 24, Last sequence update)

DT 01-UUN-2003 (TERMBLrel. 24, Last sequence update)

DT 01-UUN-2003 (TERMBLrel. 25, Last annotation update)

DF 01-UUN-2003 (TERMBLrel. 25, Last annotation update)

DF 01-UUN-2003 (TERMBLrel. 26, Last sequence update)

DF 01-UUN-2003 (TERMBLrel. 26, Last sequence update)

DF 01-UUN-2003 (TERMBLrel. 26, Last annotation update)

OC SUKaryote; Pung!; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

ON Nonicy Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NOSI TAXID-5141;

RA SCHUILte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., RA Nyakatura G., Mewes H.W., Mamhaupt G.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

RA German Neurospora genome project;

RA Golo004553; P:OAD7074011; --

DR GO: GO:0004553; P:OAD7074016; 1.

DR Ffan; PF00722; Glyco-hydrolism; IEA.

OUBSY Pfan; PF00722; Glyco-hydrolism; IEA.

DR Ffan; PF00722; Glyco-hydrolism; IEA.

OUBSY Pfan; PF00722; Glyco-hydrolism; IEA.

OUBSY Pfan; PF00722; Glyco-hydrolism; IEA.

DR GO: GO:0004504; Glyco-hydrolism; IEA.

DR GO: GO:0004504; Glyco-hydrolism; IEA.

DR GO: GO:0004504; Glyco-hydrolism; IEA.

OUBSY Pfan; PF00722; Glyco-hydrolism; IE
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Search completed: October 6, 2004, 16:33:47 Job time : 55.2632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 16:34:15 ; Search time 93.4211 Seconds (without alignments) 51.669 Million cell updates/sec	
16:34:15 ; Search (without 51.669 M	
, 2004,	744-4
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October	4-6479-63-63-6748-4
Run on:	a[+:F

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1351062 segs, 321799191 residues
                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                       1 VIWSGGNIDYNTPFT 15
.09-635-974A-4
   Perfect score:
                                                 Scoring table:
                        Sequence:
                                                                                             Searched:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUBL.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUBL.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 28, Appl	4, A	'n	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	115,	116,	Sequence 117, App	Sequence 118, App	Sequence 119, App	Sequence 120, App	Sequence 115, App	116,	Sequence 117, App
ID	US-09-798-689-28	US-09-996-954B-4	US-10-374-600-3	US-10-374-531-3	US-10-374-600-2	US-10-374-531-2	US-10-374-600-115	US-10-374-600-116	US-10-374-600-117	US-10-374-600-118	US-10-374-600-119	US-10-374-600-120	US-10-374-531-115	US-10-374-531-116	US-10-374-531-117
% Query Match Length DB	16 10	16 10	16 12	16 15	18 12	18 15	119 12	119 12	119 12	119 12	119 12	119 12	119 15	119 15	119 15
% Query Match L	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88
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	नळनंत	0000	20000	Sequence 28, Appl Sequence 29, Appl Sequence 30, Appl Sequence 13, Appl Sequence 8, Appli	sequence seq seq seq seq seq seq seq seq seq se
15 US-10-374- 15 US-10-374- 15 US-10-374- 12 US-10-374- 12 US-10-374-	38 12 US-10- 38 15 US-10- 38 15 US-10- 38 15 US-10-	32 12 US-10-374-600-2 32 12 US-10-374-600-2 32 12 US-10-374-600-2 32 12 US-10-374-600-2	32 12 US-10- 32 12 US-10- 32 15 US-10- 32 15 US-10- 32 15 US-10-	2 15 US-10-374-531-2 2 15 US-10-374-531-2 2 15 US-10-374-531-3 2 15 US-09-865-483-13 4 9 US-09-865-483-13	2 US-10-239-65 2 US-10-239-65 6 US-10-82-84 2 US-10-389-41 2 US-10-389-41 2 US-10-452-35 2 US-10-452-35
88 100.0 8 88 100.0 9 88 100.0 9 88 100.0	2 88 100.0 3 88 100.0 4 88 100.0	76.5 86.9 76.5 86.9 76.5 86.9 76.5 86.9	9 76.5 86.9 11 76.5 86.9 76.5 86.9 3 76.5 86.9	7.00 7.00 7.00 7.00 7.00 7.00 7.00 7.00	9 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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US-09-798-689-28

| Deblication No. US20030103973A1
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| APPLICANT: Goldstein, Neil I. |
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy |
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy |
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy |
| TITLE REFERENCE: Sequence Listings 1-40 |
| FILE REFERENCE: Sequence Listings 1-40 |
| FILE REFERENCE: Sequence Listings 1-80 |
| FRIOR FILING DATE: 1990-09-22 |
| FRIOR FILING DATE: 1997-11-10 |
| FRIOR FILING DATE: 1995-06-07 |
| FRIOR FILING DATE: 1994-00-20 |
| FRIOR FILING DATE: 1994-02-10 |
| FRIOR FILING DATE: 1994-03-10-10 |
| FRIOR FILING DATE: 1994-03-10 |
| FRIOR FILING DATE: 1994-04-04 |
| FRIOR FILING DATE: 1994-04-04 |
| FRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 88; DB 10; Length 16; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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US-09-798-689-28
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1 VIWSGGNIDYNIPFT 15

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Gaps ..

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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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US-10-374-531-3
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                                                                                                                Sequence 4, Application US/0996954B

Sequence 4, Application US/0996954B

Publication No US20030157104A1

GENERAL INFORMATION:

THIE OF INVENTION: Treatment of Refractory Human Tumors

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: WITH Epidermal Growth Factor Receptor Antagonists

CURRENT FILING DATE: 11245-46605

CURRENT FILING DATE: 09/09-11-30

PRIOR APPLICATION NUMBER: 09/040,146

PRIOR APPLICATION NUMBER: 09/314,028

PRIOR APPLICATION NUMBER: 09/312,284

PRIOR APPLICATION NUMBER: 09/312,284

PRIOR FILING DATE: 05-14-1999

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: IMCIONE SYSTEMS INCORPORATED, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INVENTION: INVENTION THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 88; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPES Diskrete 3.5 inch 1.44 Mb storage
COMPUTER: ISM compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION - vinknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-08 APPLICATION NUMBER: PCT/US96/09847 APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens-Rodent Chimera
US-09-996-954B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10374600
Publication No. US20030224001A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Broadway
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1 VIWSGGNTDYNTPFT 15
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STATE: New York
COUNTRY: US
                                                                                                    US-09-996-954B-4
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LENGTH: 16
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Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
ATTLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 89; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible
CORRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/08/1096/0947
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31, 995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMUNICATION INFORMATION:
TELECPHONE: (212) 425-7200
                                                                                                                                                 | TENGTH: 15 amino acids | TYPE: amino acids | TYPE: amino acid | TYPE: not relevant | MOLECULE TYPE: peptide | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-10-374-600-3
REGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425-5288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Broadway
                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNIDYNTPFT 15
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RESULT 6
US-10-374-531-2
; Sequence 2, Application US/10374531
; Publication No. US20040006212A1
; GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
; APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CUCNUIXX: US
CUCNUIXX: US
CUCNUIXX: US
CUCNITER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: LE-DEC-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: DISCOURTED AND ADDEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 88; DB 15; Best Local Similarity 100.0%; Pred. No. 1.5e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 425-5288

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL:
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
  2 VIWSGGNTDYNTPFT 16
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US-10-374-600-115
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Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
ATTLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                       Query Match
100.0%; Score 88; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READALE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible COMPUTER: Wordperfect CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: BCT/USS6/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELEBPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
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100.0%; Pred. No. 1.5e-06;
iive 0; Mismatches 0;
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                        1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                            1 VIWSGGNTDYNTPFT 15
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
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                                                                                            US-10-374-531-3
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Length 18;
                                    Indels
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Gaps
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52.10-374-600-117
5-10-374-600-117, Application US/10374600
Sequence 117, Application US/10374600
Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: IMCIONE Systems Incorporated, et al.
; TITLE OF INVENTION:
INTIBIDITING THE GROWTH OF TUMORS
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119;
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ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 88; DB 12;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIPICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
SIREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDMSS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 425-7200
TELBFAX: (212) 425-7288
INFORMATION FOR SEG ID NO: 116:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VIWSGGNTDYNTPFT 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                 ADDRESSEE: Kenyon & Kenyon STREET: One Broadway CITY: New York STATE: New York COUNTRY: US ZIF: 10004 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible COMPUTER: NEW SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
  INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 116, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/08/973,065C
RILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UW-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERRNCE/DOCKET NUBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPROKE: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 115: US-10-374-600-115
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One Broadway
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                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Matches 15; Conservative
                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
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US-10-374-600-116
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Pred. No. 1e-05;
; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IMCIONE SYSTEMS INCORPORATED, et al. TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-F6b-2003
CLASSIFICATION: cUnknown-
PRIOR APPLICATION: cUnknown-
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY, ENGRET INFORMATION:
NAME: Deborah A. SOMERVILLE
BEGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 11245/46003 TELECOMMUNICATION INFORMATION:
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 118:
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TYPE: amino acid
STYPE: amino acid
STYPE: amino acid
STANDEDNESS: not relevant
TOPOLOGY: not relevant
WOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-374-600-119
; Sequence 119, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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               TELEFAX:
                                    INFORMATION FOR
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100.0%; Score 88; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 118, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
APPLICANT: Imclone Systems FOR TITLE OF INVENTION: INFIBIONY FRAGMENTS FOR INFIBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
FILING DATE: 07-JUN-1996

APPLICATION WUMBER: US 08/482,982
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995

ATTORNEY/AGENT INFORMATION

NAME: Deborah A. Somerville

REGISTATION WUMBER: 31,995

REFERENCE/DOCKET NUMBER: 11245/46003

TELECOMMUNICATION INFORMATION:

TELEFRAX: (212) 425-7200

TELEFXX: (212) 425-588

INFORMATION FOR SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: US/08/973,065C
RILING DATE: 19-MAT-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
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REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 11245/46003
TELECOMMINICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDENNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Peb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESSE:
RADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-10-374-600-117
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STATE: New York
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TELEFAX: (212)
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                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 10004
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US-10-374-531-116
                    US-10-374-531-115
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                                        100.0%; Score 88; DB 12; Length 119; 100.0%; Pred. No. 1e-05; Live 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                             Sequence 120, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
ITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 1BM compatible
COMPUTER: 25-Feb-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION UNDRER: US/08/973,065C
PILING DATE: 19-Max-1958
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION UNDRER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION UNDRER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-5288
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 120: US-10-374-600-120
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TYPE: amino acid
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 120:
                                                                                                                                                                     50 VIWSGGNTDYNTPFT 64
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                                                                                     Conservative
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                                             Query Match
Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
US-10-374-600-119
                                                                                                                                                                                                                                        RESULT 12
US-10-374-600-120
                                                                                   15;
                                                                                        Matches
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Sequence 115, Application US/10374531
Publication Wo. US20040006212A1
GENERAL INFORMATION
GENERAL INCORPATION: ANTIBODY ERAGMENTS FOR
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INHER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 119;
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Publication No. US20040006212A1

GENERAL INFORMATION:

APPLICANT: ImClone Systems Incorporated, et al.

IITLE OF INVENTION:

INHIBODY AND ANTIBODY FRAGMENTS FOR INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 88; DB 15;
100.0%; Pred. No. 1e-05;
tive 0; Mismatches. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICATION NUMBER: US/10/374,531
PILING DATE: 25-Feb-2003
CLASSIPICATION: CUDKNOWN>
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-MET-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
FILING DATE: 15-DEC-1995
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.
Matches 15; Conservative
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100.0%; Score 88; DB 15; Length 119; 100.0%; Pred. No. 1e-05; tive 0; Mismatches 0; Indels
                                                                                        APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847 FILING DATE: 07-UTN-1996
APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-UTN-1995
APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPRONE: (212) 425-7200
TELEFRAK: (212) 425-5288
  APPLICATION NUMBER: US/10/374,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQUENCE 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 6, 2004, 17:09:03 Job time : 94.4211 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                           FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 117
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VIWSGGNIDYNTPFT 15
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Best Local Similarity 100.0
Matches 15; Conservative
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100.0%; Score 88; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVIBER OF SEQUENCES: 120
                                                                                   COMPUTER READABLE FORM:

MEDIUT TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OMPRATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 25-Feb-2003
CLASSIFICATION: CURNOWN.

PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
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ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 116: US-10-374-531-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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ADDRESSES: Kenyon & Kenyon STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 425-7200
TELEPAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
One Broadway
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US-10-374-531-117
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 6, 2004, 16:24:54; Search time 26.5789 Seconds (without alignments)
29.135 Million cell updates/sec

Title: US-09-635-974A-4

Perfect score: 88
Sequence: 1 VIWSGGNTDYNTPFT 15
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters:

389414 segs, 51625971 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

lssued_Patents_AA:*

1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/SB_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/GA_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query
No. Score Match Length DB ID

1 70 79.5 16 4 718-09-865-483-13

	Appl	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appli	455030	Appli	Appli
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Gaps

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Score 70; DB 4; Length 114; Pred. No. 0.0033; 0; Mismatches 2; Indels

Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative (

Sequence 6, Appli Sequence 7, Appli	.99	Sequence 3, Appli	21,	φ	Sequence 67, Appl	61,	m	14,	, A	Sequence 6, Appli	67	36,	4.	Sequence 5, Appli	9	7
US-08-397-411-6 US-08-397-411-7	US-08-881-037-66	US-09-189-129-3	US-08-308-494A-21	US-08-881-037-67	US-08-190-199A-67	US-08-190-199A-61	US-08-525-539A-36	US-07-942-245-14	US-08-470-139-6	US-09-347-061-6	US-09-537-911A-67	US-08-353-372A-36	US-08-652-558-4	US-08-652-558-5	US-08-652-558-6	US-08-652-558-7
73 3	97 3				22 2		31 4	107 1	11 2	11 4	•	20 2	•	•	•	20 2
54 61.4 273 54 61.4 446	3 60.2			3 60.2	3 60.2		2 59.1		2 59.1	2 59.1		2 59.1	2 59.1		2 59.1	2 59.1
7 7 7 8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 .

ALIGNMENTS

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Sequence 13, Application US/09865483

Patent No. 6680053

GREEAL INFORMATION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SI

TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
FILE REFERENCE: 1599-0197P

CURRENT APPLICATION WHORE: US/09/865,483

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-865-483-8
Sequence 8, Application US/09865483
Patent No. 6680053
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEB. Jong Wook et al.
TITLE OF INVENTION: A VARIBLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SU
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/865,483
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT (CRGANISM: Escherichia coli US-09-865-483-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Escherichia coli US-09-865-483-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserv
RESULT 1
US-09-865-483-13
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TYPE: PRT
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Score 65; DB 1; Length 119;
Pred. No. 0.018;
                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: COHEN, William P.

APPLICANT: CHENEIDER, William P.

APPLICANT: CELINCH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED INMUNOGLOBLINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READALE PORM:
COMPUTER. PELOPDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-58P-1990

PRICE APPLICATION NUMBER: US 07/310,252

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 31823-00260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/07634278; Patent No. 5530101
GENERAL INFORMATION: APPLICANT: O'MEN, Cary L. APPLICANT: CO, Man Sung APPLICANT: SCHNEIDER, William P.
                                              Sequence 60, Application US/07634278 Patent No. 5530101
                                                                                                                                                                                                                                                                            LOWINGER: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-07-634-278-61
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            RESULT 4
US-07-634-278-60
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Pred. No. 0.018;
1; Mismatches 2; Indels
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATPORNEY AGENT INFORMATION:
NAME: SMitch, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TRILECOMMUNICATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
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1 VIWSGGNTDYNTPF 14
                                   50 VIWSGGNTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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STREET: 379 _,
CITY: Palo Alto
mayTE: California
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CCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION:
US-07-634-278-37
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Gaps

50 VIWSGGSTDYNAAF 63

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LOCATION: 1..119
OTHER INFORMATION: /note= "Amino acid sequence of the
OTHER INFORMATION: heavy chain of the humanized mik-betal antibody.
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| Sequence 60, Application US/08477728
| Sequence 60, Application US/08477728
| Patent No. 585809
| GENERAL INFORMATION:
| APPLICANT: QUEEN, Cary L. | APPLICANT: SCHNEIDER, William P. | APPLICANT: SCHNEIDER, Harold E. | ITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGGLOBLINS | NUMBER OF SEQUENCES: 113 | CORRESPONDENCE ADDRESS: | ADDRESSEE: Townsend and Townsend and Crew LLP | STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto | STATE: California | COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: O'-JUN-1995
CLASSIFICATION NUMBER: US 07/634,278
FILING DATE: US 07/634,278
FILING DATE: US 07/634,278
FILING DATE: US 07/590,274
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 12-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
RESISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1919 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PATENTIN Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VIWSGGNTDYNTPF 14
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Best Local Similarity 78.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
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          APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE: 113
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08477728

Patent No. 5585089

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED INMUNOGLOBLINS NUMBER OF SEQUENCE: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                             COMPRY: US

ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, WILLIAM M
REGISTRATION NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEPHONE: (416) AMINO: 61:
FUNDAMETION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.9%; Score 65; DB 78.6%; Pred. No. 0.01 tive 1; Mismatches
                                                                                                                                                                                   STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.9
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-634-278-61
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Gaps
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; Sequence 37.
; Sequence 37.
; Retent No. 5633761
; GENERAL INFORMATION:
; APPLICANT: QUEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: ANDOLET, Nicholas F.
APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 1; Length 119;
Pred. No. 0.018;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PR PC COMPATIBLE
COMPUTER: PR PC COMPATIBLE
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: US 07/634,278
PILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
                                                                                                                                                                                         11823-002600
                    FILING DATE: 13-FBB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 11823-00260
TELECHOME: (415) 326-2400
TELEPHOME: (415) 326-2400
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                  TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-477-728-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-474-040-37
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Patent No. 5585089

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: STRICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STRIET: Talo Embarcadero Center, 8th Floor
CITY: Palo Alto
STRIET: The Embarcadero Center, 8th Floor
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 1; Length 119;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                   CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-E2P-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 18-E8-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 18-E8-1989
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
     APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-08-477-728-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SD
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US-08-477-728-61
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TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                               single
                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                      TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-474-040-61
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                /note= "Amino acid sequence of the heavy chain of the humanized mik-betal antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                  73.9%; Score 65; DB 1; Length 119; 78.6%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/474,040
FILING DATE: 07-JUN 1995
                  REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMINICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-UNY-1995
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION 536
PILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION:
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 379-Lytton Avenue CITY: Palo Alto CITY: Palo Alto STATE: California COUNTRY: US ZIP: 94301.

CONTRY: READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     TOPOLOGY: single TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.61
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                       LOCATION: 1.119
CTHER INFORMATION:
CTHER INFORMATION:
US-08-474-040-37
                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Gaps
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                                                                                                                Sequence 61, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
    APPLICANT: CO. Man Sung
    APPLICANT: SCHNSIDER, William P.
    APPLICANT: ANDOLFI, Nicholas F.
    APPLICANT: ANDOLFI, Nicholas F.
    APPLICANT: SELICK, Harold E.
    TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOCLOBLINS
    NUMBER OF SEQUENCES: 113
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
Length 119;
                                                                                                                                                                                                                                                                                                                        Score 65; DB 1;
Pred. No. 0.018;
1; Mismatches
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Gaps

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; CTHER INFORMATION: heavy chain of the humanized mik-betal antibody."
US-08-487-200-37
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                                                                                  Length 119;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                        Sequence 60, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
APPLICANT: SCHEIDEN, William P.
APPLICANT: COLLINGH, Kathleen L.
APPLICANT: SCHEILEK, Harrold E.
APPLICANT: SELICK, Harrold E.
TITLE OF INVENTION: IMPROVED HUMANIZED INMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: California
COMPUTER: California
COMPUTE: California
COMPUTE: California
COMPUTE: Eloppy disk.
COMPUTER READABLE FORM:
MIDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
COMPUTER: DetentIn Release #1.0, Version #1...
CURRANTE: PATENTIN NUMBER: US/08/487,200
APPLICATION NUMBER: US/08/487,200
FILLORITON NUMBER: US/08/487,200
FILLORITON NUMBER: US/08/487,200
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR DATE: 7-00N-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNHAR:
APPLICATION DATA:
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION UNHAR:
APPLICATION UNHAR:
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION UNHARE: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION UNHARE: 18-FEB-1989
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                     73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 119 amino acids
amino acid
                                                                                                                                                                            1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                       50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.9
Best Local Similarity 78.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-487-200-60
                                                                                                                                                                                                                                                                                         RESULT 13
US-08-487-200-60
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G
                                                                                                                                                                                   S
                                                                                                                                                         ó
                                                                                                               73.9%; Score 65; DB 1; Length 119; 78.6%; Pred. No. 0.018; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                       Sequence 3.2.3.

Sequence No. 5693762

Fatent No. 5693762

GENERAL INCRNATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Wicholas F.

APPLICANT: LANDOLFI, Micholas F.

APPLICANT: SELICK, Harold B.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMPC compatible
COMPUTER: DEACHTIN Release #1.0, Version #1.25
SUBSTRATING SYSTEM: PC-DOS/MS-DOS
SUBSTRATION NUMBER: US/08/487,200
FILING DATE: 7-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-EBB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-EBB-1999
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-EBC-1988
ATTORNEY/AGENT INFERMATION:
NAME: SMITCH WIlliam M
REGISTERATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11823-002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 119 amino acids
amino acid
                                                                                                                                                                                                           1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                        50 VIWSGGSTDYNAAF 63
                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-474-040-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserva
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/note= "Amino acid sequence of the heavy chain of the humanized mik-betal antibody."
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Sequence 37, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: CO. Man Sung
APPLICANT: ANDOLFI, Nicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.9%; Score 65; DB 3; Length 119; Best Local Similarity 78.6%; Pred. No. 0.018; Matches 11; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              ALDEADES E. 100MISEND and 100MISEND KNOWINE and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
CUNTRY: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION NABER:
US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 38-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 38-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 38-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILECOMMUNICATION NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELBFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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NAME/KEY: Protein

LOCATION: 1..119

OTHER INFORMATION: /

US-08-484-537-37
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US-08-487-200-61
US-08-487-200-61
Sequence 61, Application US/08487200
SEPPLICANT: QUEEN, Cary L.
APPLICANT: GELINGH, Mathlesn L.
APPLICANT: SELIKK, Harold E.
ITHER OF INVARION: HERROYED HUMANIZED INVUNCIOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE 3.
APPLICANT: SELIK, Harold E.
CITY: Palo Alton Aronae and Townsend and Crew
CITY: Palo Alton Avenue
COMPUTER READALD FORM:
WEDIUM TYPE: Floppy disk
COMPUTER READALD FORM:
WEDIUM TYPE: Floppy disk
COMPUTER READALD FORM:
SEPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1899
RECEISTRATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1899
RECISTRATION NUMBER: US 07/200,975
FILING DATE: US 07/200,975
FILING PARATION NUMBER: US 07/200,975
FILING PARATION NUM
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Pred. No. 0.018;
1; Mismatches 2; Indels
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Best Local Similarity 78.6%;
Matches 11; Conservative
                                          50 VIWSGGSTDYNAAF 63
1 VIWSGGNTDYNTPF 14
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MOLECULE TYPE: peptide
US-08-487-200-61
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Search completed: October 6, 2004, 16:36:31 Job time: 27.5789 secs

RESULT 15 US-08-484-537-37

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18-07-07-070-X/48-0.LD

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 6, 2004, 16:23:59 ; Search time 11.5789 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-6 62 1 ALTYYDYEFAY 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

*	Description	conserved hypothet	probable E1-E2 ATP	hypothetical prote	ы	Ig heavy chain V-D	conserved hypothet	hypothetical prote	cell division cont	D-alanine-D-alanin	-alanine	D-alanine-D-alanin	D-alanine, D-alanin	hypothetical prote	flagellar hook-ass	flagellar hook-ass	oligopeptide ABC t	proline/betaine tr	Ig heavy chain V r	conserved hypothet	cal	Н	5	ical	نڼ	probable 3-phenylp	conserved hypothet	protein-tyrosine k	a)	PK4 protein kinase
SUMMARIES		C90363	T42229	644	RRNZNV	6	8	H71697	835315	CEECDL	H90640	H85491	AG0518	T24569	G71853	G64659	E72215	C97865	F27888	F90278	T17878	AC0248	A70107	T32099	A70311	I082	300	S		813
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	Score	41	41	40	38	37	37	37		37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36
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alpha-2-macroglobu Na+-transporting A hypochetical prote E5 protein - human hypothetical prote 3-methyl-2-oxobuta hypothetical prote	phosphoenolpytrvat cyml protein - Kle hypothetical prote GTP-binding protei hypothetical protei
143166 H69862 NS4341 NSML42 T16365 G71944 G64655 E64655 B8549736 B85497	G69961 S63620 T40599 UT0741 G97272
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ALIGNMENTS

Conserved hypothetical protein [imported] - Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I., Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Cost, J.
A.Pbescription: Sulfolobus solfataricus complete genome.
A.Recession: C90363
A.Accession: C90363
A.Accession: Preliminary
A.Residues: 1-130 <KUR>
A.Residues: 1-130 <KUR>
A.Residues: 1-130 <KUR>
A.Grossereferences: GB:AB006641; NID:g13815246; PIDN:AAK42162.1; GSPDB:GN00155
C.Genetics:
A.Gene: SSO1970

Gaps 0 Length 130; 2; Indels Query Match 66.1%; Score 41; DB 2; Best Local Similarity 70.0%; Pred. No. 4.5; Matches 7; Conservative 1; Mismatches 2

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||||| :|| 89 LTYYDASYAY 98 2 LTYYDYEFAY 11

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probable E1-E2 ATPase (EC 3.6.1.-) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T42229
EXHalleck, M.S.; Blackman, C.F.; Gao, L.; Williamson, P.L.; Schlegel, R.A.
ByDescription: Multiple members of a third subfamily of P-type ATPases identified by ger
A;Reference number: 222089
A;Reference number: 222089
A;Accession: T42229
A;Accession: T42229
A;Accession: T42220
A;Accession: T42220
A;Residues: 1-1020 cHAL>
A;Residues: 1-1020 cHAL>
A;Cross.references: BMBL:AF011336; NID:g2944186; PID:g2944187; PIDN:AAC05245.1

Gaps ö Query Match 66.1%; Score 41; DB 2; Length 1020; Best Local Similarity 87.5%; Pred. No. 38; Matches 7; Conservative 0; Mismatches 1; Indels

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Gaps

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Conserved hypothetical protein [imported] - Sulfolobus solfataricus CySpecies: Sulfolobus solfataricus CySpecies: Sulfolobus solfataricus CySpecies: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 CyAccession. A90230 #sequence_revision 24-May-2001 CyAccession. A90230 #sequence_revision 24-May-2001 CyAccession. A90230 W.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Pong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Apil-Ngoc, H.P.; Redder, P. A; Description: Sulfolobus solfataricus complete genome.
A; Maccession: A99139
A; Accession: A90230
A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Gross-references: GB.AJ235271; GB.AJ235269; NID:g3868717; PIDN:CAA14858.1; PID:g3860956
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein RD401 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: 21.Nov-1998 #sequence revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: H71697
R;Andersson, S:G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUD1:99039499; PMID:9823893
A;Accession: H71697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Residues: 1-130 <KUR>
A)Cross-references: GB:AE006641; NID:g13813978; PIDN:AAK41096.1; GSPDB:GN00155 C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-247 <AND>
A;Molecule type: mRNA
A;Residues: 1-121 <REI>
A;Cross-references: EMBL:X51846; NID:g55246; PIDN:CAA36139.1; PID:g930214
C;Superfamily: immunoglobuliu v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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A;Gene: RP401
C;Superfamily: Rickettsia prowazekii hypothetical protein RP401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.7%; Score 37; DB 2; Length 130; 60.0%; Pred. No. 22; tive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                            Length 121;
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                                                                                                                                                                                                                                                                                                                  DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                       Score 37;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                       59.78;
75.08;
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                      hypothetical protein MJ1468 - Methanococcus jannaschii c) Species: Methanococcus jannaschii c) C) Species: Methanococcus species: Methanococcus c) Species: Methodococcus c) 
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: S09958
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Bur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: S09955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome polyprotein - Newcastle disease virus (strain Beaudette C)
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: Newcastle disease virus
C;Species: Newcastle disease virus
C;Accession: A26747
R;Yusoff, K; Millar, N.S.; Chambers, P.; Emmerson, P.T.
Nucleic Acids Res. 15, 3961-3976, 1987
A;Title: Nucleotide sequence analysis of the L gene of Newcastle disease virus: homologian and the contains a
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A,Residues: 1-2204 <YUS>
A,Cross-references: GB:X05399; NID:g60937; PIDN:CAA28985.1; PID:g60939
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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C,Superfamily: parainfluenza virus RNA-directed RNA polymerase
C,Keywords: ATP; nucleotidyltransferase
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Best Local Similarity 85.7
Matches 6; Conservative
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TYFDSEFSY 886
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               LKYYDYEF 718
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TYYDYEY 405
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Matches 6; Conserv
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A; Description: catalyzes ATP-driven formation of alanyl-D-alanine from 2 alanine molecul A; Description: catalyzes ATP-driven formation of alanyl-D-alanine molecul A; Pathway: cell wall synthesis A; Mote: two D-alanine-D-alanine ligases in E. coli (and S. typhimurium) encoded by two cthe two enzymes display remarkably similar catalytic efficiencies and substrate specific C; Superfamily: D-alanine-D-alanine ligase
C; Superfamily: D-alanine-D-alanine ligase motif 2
F; 245-276/Region: D-alanine-D-alanine ligase motif 2
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H90640
C alamine ligase B [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Date: 18-Jul-2001
C;Date: 18-Jul-2001
C;Date: 18-Jul-2001
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Ttle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MuID:21156231; PMID:11258796
A;Accession: H90640
A;Status: preliminary
A;Molecule type: DNA
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A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: D64731
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: 1306 ABLAT>
A/Cross-references: GB:AE000118; GB:U00096; NID:g1786262; PIDN:AAC73203.1; PID:g1786280,
A/Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                          A, Map position: 2 min
A, Mote: gene is located in a large cluster of genes that are involved in cell division
C, Function:
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A.Cross-references: GB:BA000007; PIDN:BAB33519.1; PID:g13359552; GSPDB:GN00154
A.Experimental source: strain 0157:H7, substrain RIMD 0509952
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Pred. No. 54;
1; Mismatches 2; Indels
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Pred. No. 54;
1; Mismatches
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A;Gene: EC80096
C;Superfamily: D-alanine-D-alanine ligase
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Gene: ddlB; ddl
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H85491
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A;Molecule type: DNA
A;Reaidues: 300-306 < DEW>
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                cell division control protein 16 - fission yeast (Schizosaccharomyces pombe)
(Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Dacesion: 333315; 739042
R; Fankhauser, C; Marks, J; Reymond, A.; Simanis, V.
R; Fankhauser, C; Marks, J; Reymond, A.; Simanis, V.
A; Title: The S; Dombe cdc16 gene is required both for maintenance of p34(cdc2) kinase act
A; Reference number: S35315; MUID:93327759; PMID:8334988
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A; Residues: 1-306 <ROB>
A; Residues: 1-306 <ROB>
A; Residues: 1-306 <ROB>
A; Cross-references: GB.X55034; NID:g40841; PIDN:CAA38869.1; PID:g40860
A; Cross-references: Strain K.12, substrain W3110
B; Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu submitted to the EMBL Data Library, December 1992
A; Reference number: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2
A; Reference number: S40531
A; Accession: S40602
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A,Residues: 1-306 <YUR>
A,Crestdues: 1-306 <YUR>
A,Crestdues: 1-306 <YUR>
A,Crestdues: 1-306 <YUR
B,Dewar, S.J.; Donachie, W.D.
J. Bacteriol. 172, 6411-6644, 1990
J. Bacteriol. 172, 6411-6644, 1990
A,Reference number: A37155; MUID:91035283; PMID:2228979
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N.Alternate names: alanylalanine synthetase
N.Alternate names: alanylalanine synthetase
S.Abcesia: Escherichia coli
S.Poeties: Bacherichia coli
S.Abcesion: AJ0289; AS06022, 531155; D64731
S.Rochinson, A.C.; Kenan, D.J.; Sweeney, J.; Donachie, W.D.
T. Bacteriol. 167, 809-817, 1986
A/Title: Further evidence for overlapping transcriptional units in an Escherichia coli
A/Rocession: A30289; MUID:86304170; PMID:3528126
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A Residues: 1-29 cFAND.
A;Residues: 1-29 cFAND.
A;Cross-references: EMBL:X71605; NID:g385068; PIDN:CAA50606.1; PID:g395069
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
B;Reference number: 221797
A;Reference number: 221797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-299 <GEN>
A;Cross-references: EMBL:298981; PIDN:CAB11731.1; G
A;Experimental source: strain 972h-; cosmid c6F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 52;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 1
A;Introns: 167/3; 198/1; 247/2
C;Superfamily: cell cycle arrest protein BUB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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212 ALTIWDFLFAY 222
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flagellar hook-associated protein 1 (hapl) - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: G71853
C;Accession: G71853
C;Accession: G71853
C;Gibbon, R. A., Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; I Ives, C; Gibbon, R. Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Reference number: G71853
A;Reference number: G71853
A;Residues: Jreliminary
A;Residues: 1-606 <ARN;
A;Residues: 
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Cispecies: Helicobacter pylori
Cipace: Os-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cipace: Os-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cipacession: G64659
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Boterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 389, 539-547, 1997
Mature 389, 539-547, 1997
A;Authors: Wallin, B.; Hayes, W.S.; Bordovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A;Reference number geographic of the gastric pathogen Helicobacter pylori.
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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Pred. No. 1.1e+02;
2; Mismatches 1;
Pred. No. 66;
4; Mismatches
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    ilarity 55.6%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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41 AMTHYDFDF 49
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TYYDTEFSH 94
                                                                                                                                      1 ALTYYDYBF
    Best Local Similarity
Matches 5; Conserv
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AG0518
AG0518
C. Calanine ligase B [imported] - Salmonella enterica subsp. enterica serovar Ty
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0518
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, A.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Accession: AG0518
A;Accession: AG0518
A;Accession: AG0518
A;Accession: Preliminary
A;Accession: Dava
A;Accession: H85491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <STO>
A;Cross-references: GB:AE005174; NID:g12512798; PIDN:AAG54396.1; GSPDB:GN00145; UWGP:Z01
A;Experimental source: strain O157:H7; substrain EDL933
C;Genetics:
A;Gene: ddlB
C;Superfamily: D-alanine-D-alanine ligase
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T24569
T724569
Hypothetical protein T06C12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T24569
R;Kelly, P.
Submitted to the REBL Data Library, October 1996
A;Reference number: Z19908
A;Accession: T24569
A;Accession: T24669
A;Accession:
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A,Residues: 1-306 <PAR>
A,Cross-references: GB:AL513382; PIDN:CAD01287.1; PID:g16501415; GSPDB:GN00176
C,Genetics: A,Gene: STY0150
C;Superfamily: D-alanine-D-alanine ligase
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A/Map postition: A/Map postition: 66/2; 290/3
A;Introns: 66/2; 290/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C36C9.3
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Pred. No. 54;
1; Mismatches 2; Indels
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54;
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Pred. No.
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ilarity 66.7%;
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Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 6, 2004, 16:21:13 ; Search time 6.75439 Seconds (without alignments) 84.800 Million cell updates/sec

US-09-635-974A-6 62 1 ALTYYDYEFAY 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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HELL VZVD SLAP THETH PYP RHOSH YG34 BPLLH YG34 BPLLH YG34 BPLLH YG34 BPLLH YB56 SULSO YB56 SULSO YB56 SULSO YB56 SULSO YB57 SERVE DDL NEIMB DDL NEIMB DDL NEIMB DDL BENESAU DDL BESAE
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Matches 6; Conservative
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  6; Conservative
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                                                                                                            399 TYYDYEY 405
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                                                    3 TYYDYEF 9
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ID Y401_RICPR
AC Q9ZDD0;
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RRPL NDVB
ID RRPL NDVB
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SEQUENCE FROM N.A.
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 5 PKD domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; InterPro; PRD.
Pfam; PF00801; PKD.
SMART: SMOO89; PKD; 5.
PROSITE: PS50093; PKD; 5.
Hypothetical protein; Transmembrane; Repeat; Complete proteome.
TRANSMEM 6 26 POTENTIAT.
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                                                                                                                                          Score 43; DB 1; Length 358; Pred. No. 3.4; 0; Indels 1; Mismatches 0; Indels
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                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
7B73FAB7A3BC3670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea, Buryarchaeota, Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein MJ1468.
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POTENTIAL.
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PKO 4.
PKO 5.
                                                                                           41623 MW;
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85.7%;
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                                                                                                                                                   69.4%;
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                                                                                                                                                                          87.5%;
                                                                                                                                                                       Best Local Similarity 97.5
Matches 7; Conservative
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                                                                                           358 AA;
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                                                                   DOMAIN
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01-UTL-1989 (Rel. 11, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function in mRNA synthesis, capping, methylation and poly(A) synthesis of newly synthesized viral mRNAs, RNA editing of the Isynthesis of the Natural Synthesis of the Synthesis of the Synthesis of the Synthesis of the Synthylic Activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=87320982; PubMed=3035486;

Yusoff K., Millar N.S., Chambers P., Emmerson P.T.;

"Nucleotide sequence analysis of the L gene of Newcastle disease
"Nucleotide sequence analysis of the L gene of Newcastle viruses.";

"Nucleotide sequence analysis of the L gene of Newcastle disease
"Nucleotide sequence analysis of the Light stomatitis viruses.";

Nucleic Acids Res. 15:3961-3976(1987).

-I- FUNCTION: Probable component of the active polymerase. It may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
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Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 2204;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007098; RNA_pol_monon.
InterPro; IPR01016; Viral_RNA_pol_L.
Pfam; PF00946; Paramyx_RNA_pol_1.
Transferase; RNA-directed RNA_polymerase.
SEQUENCE 2204 AA; 248822 MW; C67B8674D904802C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newcastle disease virus (strain Beaudette C/45) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
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ID DDLB_ECOS7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-216, Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Asgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Honrsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Amoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'nell S., Mungall K., Murphy L., Stablinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE 93327759; PubMed=8334988;
Fankhauser C., Marks J., Reymond A., Simanis V.;
"The S. pombe cdc16 gene is required both for maintenance of p34cdc2
kinase activity and regulation of septum formation: a link between
mitosis and cytckinesis?"
EMBO J. 12:2697-2704(1993).
                                                                Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
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                                                                                                                                                                                                                                                                                                                                    59.7%; Score 37; DB 1; Length 247;
85.7%; Pred. No. 25;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    EMBL; AJ235271; CAA14858.1; -.
PIR; H1687; H71697.
HYpothetical protein; Complete proteome.
SEQUENCE: 247 AA; 28125 MW; A30702F1912543D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Pungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CDC16 OR SPAC6F6,08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 AA
                                       STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 85...,
6; Conservative
                                                                                                                                   Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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NCBI_TaxID=4896;
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                 Weltjens I., Vanetreels E., Relear M., Schaefer M., Mueller-Auer S., Agbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Babel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Geffeu A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Hith Genome Sequence of Schizosaccharomyces pombe.";

"The Stallary Regulars Pop Redulation of Septim Formation C. Involued IN MAINTENANCE OF CDC2 KINASE ACTIVITY IT IS

SUBSEQUENTLY REQUIRED FOR REGULATION OF SEPTIM FORMATION.

CONTRIBECTLY OR INDIRECTLY THE DESCRAPATION OF CYCLIN OR THE DEPHOSPHORYLATION OF THE TEST CONTRIBENCE.

CONTRIBECTLY OR INDIRECTLY THE DESCRAPATION OF CYCLIN OR THE DEPHOSPHORYLATION OF THE TEST CONTRIBENCE.

CONTRIBENCE THE TEST CONTRIBENCE OF THE TEST CONTRIBENCE.

SIMPLARITY: Contains I Rab-GAP TBC domain.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
D-alamine--D-alamine ligase B (EC 6.3.2.4) (D-alanylalanine synthetase B) (D-Ala-D-Ala ligase B).
Escherichia coli OLS-RS-0096.
Bacteria, Proteobbacteria, Gammaproteobacteria; Enterobacteriales,
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
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Robben J
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InterPro; IPR000195; RabGAP_TBC.
Pfam; PF00566; TBC; 1.
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EMBL; Z98981; CAB11731.1; -.
PIR; S35315; S35315.
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212 ALTIWDFLFAY 222
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207 TFYDYEAKY 215
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DDLB ECOLI
ID DDLB ECOLI
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                                                                                                                                                                                                                                                                                            Gaps
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                           enterohaemorrhagic Escherichia coli O157:H7.";
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation u
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1; Mismatches
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InterPro; IPR00505; D ala D ala.
InterPro; IPR000291; Dala Dig_van.
Pfam; PF01820; Dala Dala Ligas; 1.
TGRAPM; TGR01925; D ala D alaTICR; 1.
PROSTIE; PS00843; DALA DALA LIGASE 1: 1.
PROSTIE; PS00844; DALA DALA LIGASE 2: 1.
                                                                                                                                                              (2)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; Pubmed-11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE005186; AAG54396.1; -. BMBL, AF002550; BAB33519.1; -. PIR, H85491, H85491. PIR, H90640.
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                                                                                      "Genome sequence of enter
Nature 409:529-533(2001).
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Matches 6, Conservative
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Q8FL63;
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DDLB_ECOL6
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               Gaps
                                                                                                                                                                                                                                                                                       alanyl-D-alanine.
                                                                                                                                                                                                                                                                                                                                                                   -!- SUBENIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome
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01-ARF-1993 (Rel. 25, Last sequence update)
10-07-2003 (Rel. 25, Last sequence update)
0-alanine-D-alanine ligase B (EC 6.3.2.4) (D-alanine Synthetase B) (D-Ala-D-Ala ligase B).
05-Alanine ligase B) (D-Ala-D-Ala ligase B).
05-Alanine Sobre (Boogs)
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Pred. No. 31;
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HAMAP; MF 00047; -; 1

R InterPro; IPR002905; Dala lig Van.

R PGam; PF01820; Dala Dala lig Van.

R TICRFAM; TICR01205; Dala lala larigs; 1.

R ROSITE; PS00843; DALA DALA LIGASE 1; 1.

DR ROSITE; PS00844; DALA DALA LIGASE 2; 1.

KW Ligase; Cell wall; Peptidoglycan synthesis; FT INIT MST 0 0 BY SIMILARITY.

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MEDLINE=22388234; PubMed=12471157;
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MEDLINE=86304170; PubMed=3528126;
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hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     Ikeda M., Wachi M., Jung H.K., Ishino F., Matsuhashi M.;
"Nucleotide sequence involving murG and murC in the mra gene cluster
region of Escherichia col!";
Nucleic Acids Res. 18:4014-4014(1990).
                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Shao Y.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
science 277:1453-1474(1997).
 sequence and transcriptional organization of the ddl ftsQ region."; J. Bacteriol. 167:809-817(1986).
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                                                                                          Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia coli genome: analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-95025539; PubMed=7939684;
MEDLINE-95025539; PubMed=7939684;
MEDLINE-95025539; PubMed=7939684;
"Van Co., Mows P.C., Walsh C.T., Knox J.R.;
"Van Comycin resistance: structure of D-alanine:D-alanine ligase at 2.3-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBGNIT: Monomer.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
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MEDLINE=97207065; PubMed=9054558;
Fan C., Park I.-S., Walsh C.T., Knox J.R.;
"D-alanine:D-alanine ligase: phosphonate and phosphinate
intermediates with wild type and the Y216F mutant.";
Biochemistry 36:2531-2538(1997).
-!- FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-alanyl-D-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92207163; PubMed=1554356; Albar O.A., O'Connor C.D., Giles I.G., Akhtar M.; "D-alanine-D-alanine ligase of Escherichia coli. Expression, purification and inhibitory studies on the cloned enzyme."; Biochem. J. 282:747-752(1992).
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                                                                                                                                        the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                               MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90326550; PubMed=2197603;
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EMBL; K02668; AAA23815.1; --
EMBL; X52644; CAA36869.1; --
EMBL; X55034; CAA38869.1; --
EMBL; D10483; BAB96660.1; --
EMBL; AB000118; AAC73203.1; --
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-40 FROM N.A. STRAIN=K12;
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                                           SEQUENCE FROM N.A.
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Score 37; DB 1; Length 305;
Pred. No. 31;
1; Mismatches 2; Indels
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ilarity 66.7%;
Conservative
                                                                                                                                                                          305 AA;
                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                    Matches
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TYYDYEFAY 11

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Gaps

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DDLB_SALTY
       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tarkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Tompiece genome sequence of a multiple drug resistant Salmonella enterica servora Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=TY2 / ATCC 700931; MEDIAGE 12644504; MEDIAGE 2531367; PubMed=12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF 00047; -; 1.

InterPro; IPR005905; D ala D ala.

InterPro; IPR00291; D ala Iigas.

FrancePro; IPR00291; D ala Iigas; 1.

TIGRPAMS; TIGR01205; D ala D alaTIGR; 1.

PROSITE; PS00843; DALA DALA LIGASE 1; 1.

PROSITE; PS00844; DALA DALA LIGASE 2; 1.

Inigase; Cell wall; Peptidoglycan synthesis; Complete proteome.

INIT MET.

O BY SIMILARITY.
                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-COT-2003 (Rel. 42, Last annotation update)
10-Alanine -D-alanine ligase B (EC 6.3.2.4) (D-alanylalanine synthetase B) (D-Ala-D-Ala ligase B).
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                                                                                                                                                                                   305 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Salmonella, NCBI TaxID=601;
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              207 TFYDYEAKY 215
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Best Local Similarity
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0829G7;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Layman D., Courtney L., Powollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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--- SUBUNIT: Monomer (By similarity)
--- SUBUNIT: MOLOATION: Cytoplasmic (By similarity)
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
--- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
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InterPro; IPR005905; D ala D ala.
InterPro; IPR005905; D ala D ala.
InterPro; IPR005915; Dala Iligas; 1.
IIGRPAMS; TIGR01205; D ala D alaTIGR; 1.
PROSITE; PS00844; DALA DALA LIGASE_1; 1.
PROSITE; PS00844; DALA DALA LIGASE_2; 1.
Ingase; Cell wall; Peptidoglycan synthesis; Complete proteome.
INIT_MET
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10-0CT-2003 (Rel. 42, Last annotation update)
D-alanine--D-alanine ligase B (EC 6.3.2.4) (D-alanylalanine synthetase B) (D-Ala-D-Ala ligase B).
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Pred. No. 31;
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les 6; Conservative
                                                                                                                                                                                                                                  STANDARD;
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Salmonella typhimurium.
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                                                              207 TPÝDÝBAKÝ 215
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3 TYYDYEFAY 11
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RESULT 11

Euteleostomi;

Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (Human)

NCBI_TaxID=9606;

SEQUENCE OF 15-1047 FROM N.A. (ISOFORM SHORT)

AT9A HUMAN STANDARD; PRT; 1047 AA.
075110; Q9NOK6; Q9NQX;
130-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase IIA (EC 3.6.1.-).
ATP9A OR KIAA0611.

DDLB SHIFL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yuan E., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
VCDI_TaxID=623;
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EMBL; AE01678; AAP15635.1;

INTERPORT: 1.

INTERPORT
                                   Q83MF7; Q70DS4; C70DS4; C70DS5; C70DS5
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     306 AA
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     PRT;
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Best Local Similarity 66.7
Matches 6; Conservative
     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Shigella flexner
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SEQUENCE FROSTRAIN=301 ,
SHIFL
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                                         SO TENT TO THE TRANSPORT OF THE TRANSPOR
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RN 520 GOURGE FROM N.A. (ISOFORMS LONG AND SHORT).

RY ABOLINE-21638749; PubMed-11780052;

KR DELINE-21638749; PubMed-11780052;

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Basiley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,

RA Basiley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,

RA Chapman J.C., Clamp M., Clark G., Carter N.P.,

Clark G.V., Carter N.P.,

Clark G.V., Carter N.P.,

RA Chapman D.V., Carlefiths R.B., Connor R.E., Corby N.R.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Oriffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle E., Hunt A.R., Hunt S.E., Yekosch K., Johnson D.,

RA KAY M.P., Kimberley A.M., King A., Knights A., Jahrd G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay B.N., Lovell J.D.,

RA Mine S.A., Mistry D., McConnachie L.J., McLay H., Rawlor S.,

RA Mine S.A., Mistry D., McConnachie L.J., Nore M.Y. Ray P.N., Ranger B.N., Troet C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Swann R.M., Sycamore N., Taylor R., Thee, Shown, Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,

RA Wiltehead S.L., Whittaker P., Willey D.L., Williams S.A.,

RA Horer J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rocer J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=075110-2; Sequence=VSP_000412; SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=99403880; PubMed=9734811;
IShlkawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomira N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
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IsoId=075110-1; Sequence=Displayed;
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Nature 414:865-871(2001)
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Gaps

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Indels

Pred. No. 31; 1; Mismatches

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Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D.,
Williamson P., Schlegel R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                               InterPro; IPR001757; ArPase E1-E2.
InterPro; IPR001757; ArPase E1-E2.
InterPro; IPR00539; Flippase.
InterPro; IPR0053914; Hydrolase.
Pfan; Pr00109; Hydrolase; 1.
Prospins; Pr00119; CATATPASE; 1.
TIGRPAMs; TIGR01652; ATPase-Plipid; 1.
TIGRAMs; TIGR01494; ArPase-P-type; 7.
Hydrolase; Transmembrae; Phosphorylation; Magnesium; ATP-binding; Alternative Splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
Missing (in isoform Short).
/FIId-VSP_000432.
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070028; Q8VDIS; Q922L9;
30-MAY-2000 (Rel. 39, Last sequence update)
10-00T-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase IIA (EC 3.6.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%; Score 37; DB 1; Length 1047; 75.0%; Pred. No. 1.1e+02; ive 1; Mismatches 1; Indels
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                                          EMBL; AL138807; CAB92773.1; -.
EMBL; AL035684; CAB63450.1; -.
EMBL; AL138807; CAB92774.1; ALT_SEQ.
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                                                                                                              Genew; HGNC:13540; ATP9A.
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                                 SEQUENCE OF 28-1047 FROM N.A.
MEDLINE-99217376; PubMed-9548971;
Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
Schlegel R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation, Magnesium, ATP-binding,
Differential expression of putative transbilayer amphipath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
TIGRRAMS; TIGR01652; ATPASE-Plipid; 1.
TIGRPAMS; TIGR01494; ATPASE_P-type; 7.
PROSITE; PS001164; ATPASE_E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylati
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF152243; AAF08396.1; -.
EMBL; BC01336; AAC05245.1; -.
EMBL; BC006914; AAAC1814.1; -.
EMBL; BC006919; AAH06949.1; -.
PIR; T42229; T42229.
MGD; MGI:1330826; App9a.
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR005839; Flippase.
                 Physiol. Genomics 1:139-150(1999).
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          transporters.";
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REMEL; U28766; AABS33930.1; -.

REMEL; AZ0107; AZ0107

RESP: PODS62; IGD1.

RESP: 
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Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
"The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.",
                                                                                                                  + phosphate
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                                                               Nature 390:580-586(1997).

-!- CATALYTY: ACTIVITY: D-glyceraldehyde 3-phosphate + pho-
-!- NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBGINIT: Homotetramer (By similarity).
-!- SUBGINIT: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.1%; Score 36; DB 1; Length 335; 60.0%; Pred. No. 50; 1tive 2; Mismatches 2; Indels
   sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 294 A -> P (IN REF. 1).
4 294 S -> P (IN REF. 1).
AA, 36254 MW, 30E94F988339819C0 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_113 precursor.
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MEDLINE=98196666; PubMed=9537320;
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Aquifex aeolicus.
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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V -> I (IN REF. 3).

V -> I (IN REF. 3).

V -> E (IN REF. 3).

K -> E (IN REF. 2).

R -> K (IN REF. 2).

R -> K (IN REF. 2).

R -> E (IN REF. 3).

C -> P (IN REF. 3).

S -> C (IN REF. 3).

S -> C (IN REF. 3).

ALVOUTE -> TLAGKEG (IN REF. 2; AAH21814).

V -> I (IN REF. 3).

ALVOUTE -> D (IN REF. 3).

H -> D (IN REF. 3).

E -> D (IN REF. 3).
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STRAINS_ATCC 35210 / B31;
STRAINS_B8065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.P., Fleischmann K.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salchardson D.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Ulterbock T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] — SEQUENCE FROM N.A. SIJ, SEQUENCE FROM N.A. STRAIN-ATICC 35210 / B31, MEDLINE=96110942; PubMed=8557349; Anda P., Gebbia J.A., Backenson P.B., Coleman J.L., Benach J.L.; Anda P., Gebbia J.A., backenson P.B., Coleman J.L., Benach J.L.; burgdorferi and Borrelia hermsii."; Infect. Immun. 64:262-268(1996).
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1946795; O510B4;
01-NOV-1995 (Rel. 32, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
G1yceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GAP OR BBOG57.
                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
R -> K (IN REF. 3).
V -> I (IN REF. 3).
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
                                                           EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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75.0%;
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1047 AA;
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Search completed: October 6, 2004, 16:30:25 Job time: 7.75439 secs

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October 6, 2004, 16:23:13; Search time 36.8596 Seconds (without alignments) 94.160 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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| SP_archea:*
| SP_bacteria:*
| Sp_tungi:*
| Sp_tungi:
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Gapop 10.0 , Gapext 0.5
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62
1 ALTYYDYEFAY 11
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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		Description	2813q3 plasmodium	O8p041 streptococc	OBkeno streptococc	Q97wy9 sulfolobus	28e3êl streptodoc	O8dxs1 streptococc	2860w8 mus musculu	385zw9 mus musculu	3857e5 mycobacteri	29cv82 mus musculu	Q89y18 bacteroides	09emu7 amsacta moc	28xle4 clostridium	O8p7x5 xanthomonas	08jqw5 rana ridibu	884j3 encephalito
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		DB	ហ	16	16	17	16	16	۲	7	σ	11	16	12	76	16	13	S
		Match Length DB	2054	259	259	130	210	210	323	329	77	495	580	148	154	255	333	465
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Q93wc0 hordeum vul Q89q19 bradyrhizob Q87jt1 vibrio para Q8njt1 vibrio para Q8njt1 mono sapien	8 gar 1 gar		sulto svrob	Q80bt9 spedoptera Oganw9 bacteroides	Q83mf7 shigella fl Q7uds4 shigella fl		QBawx8 gadus morhu Q90z48 oncorhynchu	Q90zfl oncorhynchu O18043 caenorhabdi	8 9	4	Q858zl bacteriopha	Q88es2 pseudomonas
Q93WC0 Q89QL9 Q87JT1 Q8NB73	009498 Q8QXX1 O55601	09PXA8 09PXA7	Q9UXI4 Q9UXI4 Q8ZUJ3	Q80BT9 O9ANW9	Q83MF7 Q7UDS4	Q89EI3 Q9PTW5	Q8AWX8 Q90Z48	Q90ZF1 O18043	Q9AM03	025744	085821	Q88ES2
0 H H 4 4	122	155	17	175	16 16		13	m	16		V	16
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Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A., Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M., Hayashi H., Hamada S., Inthe Mayashi H., Hamada S., Inthe Mayashi H., Hamada S., S., Submitted Ginvasive Streptococcus pyogenes; a comparative analysis of S. pyogenes SSI-1, SF370 and MGASB332."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AR014161, AAM79879.1; SEMBL, AP0051415; BACG3685.1; Hypothetical protein; Complete proteome. SEQUENCE 259 AA; 30337 MW; 7088BBEE221C8D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINMATCC 35092 / DSM 1617 / P2;
STRAINMATCC 35092 / DSM 1617 / P2;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doollittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon, Sulfolobus solfataricus P2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus solfataricus.
Archaea, Crenarchaeota, Thermoprotei; Sulfolobales, Sulfolobaceae;
Sulfolobus.
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Pred. No. 22;
1; Mismatches 2; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 130 AA, 15106 MW; SBOB966B366BD159 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A. 98:7835-7840(2001).
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01-MAR-2003 (TrEMBLrel. 23, Created)
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EMBL, AE006804; AAK42162.1; -
PIR, C90363; C90363; Interpro; IPR002716; PIN.
Interpro; IPR00596; PINC.
Pfam; PF01850; PIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein SSO1970.
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                                                                        STRAIN-SSI-1 / Serotype M3;
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Best Local Similarity 70.vv,
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Best Local Similarity 70...
7; Conservative
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LTYYDASYAY 98
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01-OCT-2001 (
01-JUN-2003 (
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Q8E3E1
ID Q8E3E
AC Q8E3E
DT 01-MA
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Q97WY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22133808; PubMed=12122206; Berctype M3; Berces S.B., Sylva G.L., Barblan K.D., Lei B., Hoff J.S., Barkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Cornievert P.M., Musser J.M.; Ghievert P.M., Musser J.M.; eguence of a serotype M3 strain of group A Streptococcus: emergence.";
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                                                    Length 2054;
                                Score 44; DB 5; Length 203-
Pred. No. 1.3e+02;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SpW3_1272.
8PW3_1272 OR SPS0590.
Streptococcus pyogenes (serctype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
       2054 AA; 244096 MW; 522D7E233ACD1D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
EMBL, AE010071; AAL98141.11; -
Hypothetical protein; Complete proteome.
SEQUENCE 259 AA; 30329 NW; 40790BA21E3AC18B CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein spyM18_1578.
                                                                                                                                                                                                                                                                                                                   259 AA.
                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                       71.0%;
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Matches 7; Conservative
                                                                             Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                               1046 LTYYDYNYDY 1055
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                   2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=186103;
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          SEQUENCE
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Q8P041
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SECONDARY STANDARY ST
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Major histocompatibility complex class Ib M10.1 (Fragment).
                        66.1%; Score 41; DB 16; Length 210; 60.0%; Pred. No. 39; 1; Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 -1
SEQUENCE 323 AA; 37016 MW; CDDB8C3C1D816828 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Histocompatibility 2, M region locus 10.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.5%; Score 40; DB 7; 87.5%; Pred. No. 89; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] -
SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUE=Vomeronasal organ;
MEDLINE=22507899; PubMed=12620187;
                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                         2 LTYYDYEFAY 11
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12 LTYFEYDFDY 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 LTÝYGYEF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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Q852W9;
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STRAIN=2603 V/R / Serotype V;

STRAIN=2222988; PubMed=1220647;

MEDLINE=2222988; PubMed=1220647;

MEDLINE=2222988; PubMed=1220647;

Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewifs M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,

Praser C.M.,
                                                                                                                                                                                                            STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                               Kunst F.;
"Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 16; Length 210;
Pred. No. 39;
3; Mismatches 1; Indels
                                                                                   Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                 Sagalist; gbs1818; -.
InterPro; IPR007373; TPK_B1_binding.
InterPro; IPR007371; TPK_Catalytic.
Pfam; PF04265; TPK_B1_binding, 1.
Pfam; PF04265; TPK_Catalytic; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 210 AA; 23835 MW; 203E6B6FEBC81638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007373; TPK Bl binding.
InterPro; IPR007371; TPK catalytic.
Pfam; PF04265; TPK Bl binding; 1.
Hym. PF04263; TPK catalytic; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 210 AA; 23890 MW; 7F9B91304E37B63E CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
4-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
4-Ypothetical protein.
GBS1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     invasive neonatal disease.",
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766853; CAD47477.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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LTYFEYDFDY 21
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                                                                                                                                                 NCBI TaxID=216495;
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                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                             Streptococcus.
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QBDXS1
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Conserved hypothetical protein.
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Best Local Similarity 66.7%;
Matches 6; Conservative
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NCBI_TaxID=10090;
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Q89YL8
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Ishii T., Hirota J., Mombaerts P.; "Combinatorial Coexpression of Neural and Immune Multigene Families in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=2292660; PubMed=12705866;

Pedulla M.L., Ford M.B., Houtz J.M., Karthikeyan T., Wadsworth C.,

Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pamunzio N.R.,

Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,

Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,

Hatfull G.F.,

"Origins of highly mosaic mycobacteriophage genomes.";

"Origins of highly mosaic mycobacteriophage genomes.";

EMBL, AX12932; AANON331.1; -.

SEQUENCE 77 AA, 8809 MW; B8D295DB02C82ED6 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacteriophage Bxz2.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCEI_TaxID=205870;
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                                                                                                                                                                                                                                                                                                                      01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
2310003L06Rik protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                    Mouse Voneronasal Sensory Neurons.";
Curr. Biol. 13:394-400 (2003).
EMBL, AFS59598, AAG5021.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig-li.
InterPro; IPR003069; Ig-MHC.
InterPro; IPR003069; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 87.5
Matches 7, Conservative
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09CV82
DD 09CV8
DT 01-JU
DT 01-JU
DE 23100
GN 23100
GN 23100
GN EMBE
OC EMBE
MAMME
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2085785
AC 0857
AC 0857
DT 01-J
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ENGINECE FROM TAILSTEEFONGUE;

RA MENDINESCENE/GI, TAISSHEEFONGUE;

RA AZEWAR T. Hara A. P. Rhindra K., Yoshino M., Itoh M., Ishii Y.,

RA AZEWAR T. Hara A., P. Rhindra K., Yoshino M., Itoh M., Ishii Y.,

RA AZEWAR T. Hara A., P. Rhindra K., Yoshino M., Itoh M., Ishii Y.,

RA AZEWAR T. Hara A., P. Rhindra H., Yoshino H., Kandara T., Fastic R.,

RA AZEWAR T. Hara A., P. Rhindra H., Yoshino H., Kandara T., Fastic R.,

RA AZEWAR T. AZEWAR M. N. SEMI K. M. SEMI K., RONGO S., Tamanaka I.,

RA AZEWAR T. AZEWAR M. N. SEMI K. M. SEMI K. M. KANDER T.,

RA RAILO T., Olasaka H. A., Rabinar G. S., M. SEMI K.,

RA SAMI K., Olido T., Puruo M., Anno H., Madra T., Washo T.,

RA SAMI K., Olido T., Puruo M., Anno H., Baldardi R.,

RA SAMI K., Olido T., Puruo M., Anno H., Baldardi R.,

RA DASHINGTON T., BRIC C., PICERE C., TONICE M. OSTION R.,

RA DASHINGTON T., BRIC C., PICERE C., TONICE M. CARLINGH M.,

RA DASHINGTON T., BRIC C., SPECHER C., TONICE M. CARLINGH M.,

RA DASHINGTON T., BRIC C., SPECHER C., TONICE M. CARLINGH M.,

RA DASHINGTON T., BRIC C., SPECHER C., TONICE M. CARLINGH M.,

RA DASHINGTON T., BRIC C., SPECHER C., TONICE M. CARLINGH M.,

RA WINNER A. SAN S. M. SAN S. M. SAN S. M., RANDA M.,
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Nature 4177459-463 (2002).
EMBL, AB012359; AAM41756.1; -.
GO, GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004357; IVSec_cagX.
Effam; PF03524; cagX; 1.
Complete proteome.
SEQUENCE 255 AA, 29205 MW; FD0C8C0:
                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%;
66.7%;
                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.,
Best Local 6, Conservative
                                                                           PRELIMINARY;
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2 LIYYDYEFAY 11
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                   LTLYDYELDY
                                                                                                                                 VirB9 protein.
VIRB9 OR XCC2480.
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Q8JGWS
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                 Amsacta moorei entomopoxvirus (AmEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
VNCBI_TaxID=28321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtanni K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hartori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium perfringens.
Bacceria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                     "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus: Analysis and Comparison with Other Poxviruses."; Virology 274:120-139(2000).
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0
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,

MOYDER R.W.,

MOYDER R.W.,

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF250284; AAG02808.1; --

SEQUENCE 148 AA; 18636 MW; DAA4C41A79AF04DZ CRC64;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20396580; PubMed=10936094;
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
Moyer R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.3%; Score 38; DB 16; Length 154; 70.0%; Pred. No. 89; 21ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 12; Length 148;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003189; BAB6084.1; -
Hypothetical protein; Complete protecme.
SEQUENCE 154 AA; 17870 MW; E8370264C4F9B7A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE1098.
                                                                                                          Last sequence update)
Last annotation update)
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                                                                            148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                 Created)
                                                                           PRT;
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50.0%;
                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.v.
S; Conservative
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Best Local Similarity 70.v-
                                                                           PRELIMINARY;
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137 MEYYDYKYIY 146
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                  162 TYYDYPRAY 170
 3 TYYDYEFAY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flesh-eater.";
                                                                                                                                 AMV102.
                                                                          09EMU7
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                                                   RESULT 12
Q9EMU7
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[1]
SEQUENCE FROM N.A.
TISSUE=Pituitary;
Peinado J.R., Castano J.P., Sanchez-Hormigo A., Anouar Y., Tonon M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rana ridibunda (Laughing frog) (Marsh frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
NCBI_TaxID=8406;
                                                                                                            Xanthomonas campestris (pv. campestris).Bacteria; Yroteobacteria; Gammaproteobacteria; Xanthomonadales;Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
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Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 AA; 29205 MW; FD0C8C0570E8B71C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AA.
255 AA
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RA Vaudry H., Gracia-Navarro F., Malagon M.M.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

C. --CATALVITC ACTIVITY. D-GLYCERALDEHYDE 3.PHOSPHATE + PHOSPHATE + PHOSPHATE + NADH.

CC --- SUBCALVICEROUS PHASE OF GLYCOLYSIS; FIRST STEP.

CC --- SUBCOLTION: CYTOPLASHITY).

CC --- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3.PHOSPHATE

CC --- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3.PHOSPHATE

CC --- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3.PHOSPHATE

CC --- SIMILARITY: BILONGS TO THE GLYCERALDEHYDE 3.PHOSPHATE

DR GO; GO:0006495; F:Glycoraldehyde-3-phosphate dehydrogenase (p. .; IEA.

DR GO; GO:0006495; F:Glycoraldehyde-3-phosphate activity; IEA.

DR HORPIC: PRO00642; GAPDH-I:

DR Ffam; PF000644; GAPDH-I:

DR Ffam; PF00644; GAPDH-I:

DR Ffam; PF00644; GAPDH-I:

DR Ffam; PF00644; GAPDH-I:

DR Ffam; PF00644; GAPDH-I:

DR FFAM; PRO0071; GAPDH-I:

DR FFAM; PRO0071; GAPDH-I:

COLORY MATCHE 333 AA; 35679 WW; 0A93AA634C8974FC CRC64;

COLORY MATCHES 6; CONSERVATIVE 2; MISMATCHES 2; Indels 0; Gaps 0;
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Search completed: October 6, 2004, 16:33:52 Job time : 41.8596 secs

2 LTYYDYEFAY 11 :|:|| || || 309 ITWYDNEFGY 318

QQ

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Description	Sequence 30. Appl	9	Ξ	Ħ	O	66	115	Sequence 116, App		118,	Sequence 119, App	Sequence 120, App	Sequence 115, App	Sequence 116, App	Sequence 117, App	
QI.	US-09-798-689-30	US-09-996-954B-6	US-10-374-600-111	US-10-374-531-111	US-10-374-600-99	US-10-374-531-99	US-10-374-600-115	US-10-374-600-116	US-10-374-600-117	US-10-374-600-118	US-10-374-600-119	US-10-374-600-120	US-10-374-531-115	US-10-374-531-116	US-10-374-531-117	
DB	101	10	12	15	12	15	12	12	12	12	12	12	15	15	15	
Query Match Length DB	11	11	11	11	13	13	119	119	119	119	119	119	119	119	119	
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
Score	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	
Result No.	7	61	m	4,	Ŋ	9	7	α	σ	10	11	12	13	14	15	

1 ALTYYDYEFAY 11

equence 11	equence 119,	equence 12	œ	13	equence 19	80	13	e 19	24	26	27	28	29	equence 30	24	26	equence 27	28	29	30	78,	e 79,	e 41	_	equence 24	7	4.	2	Sequence 1, Appli
US-10-374-531-1	-10-374-531-11	US-10-374-531-1	US-10-374-600-	US-10-374-600-1	US-10-374-600-	US-10-374-5	US-10-374-5			US-10-374-600-2	US-10-374-6	US-10-374-600-2	US-10-374-6	US-10-374-600-3	US-10-374-531-	US-10-374-531-2	US-10-374-531-2	.5 US-10-374-531-28	US-10-374-531-	US-10-374-531-3	US	US-09-905-243-7	6 US-10-767-701-41	-10-437-963-11	US-10-104-047-24	us-	0-372-735	4 US-10-234-57	US-09-839-666-1
119 1	119	119	138 1	138 1	138 1	138 1	138 1	138 1	132 1	132 1	132 1	132 1	132. 1	132 1	132 1	m	132 1	E	m	(L)	18	Н	95	g	-	13 9	13 1	m	14 9
2 100.	62 100.0	Z 100.	2 10	100	2 10	N														80	0	0	8	œ	8	37 59.7	7	_	37 59.7
16	17	87	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

GENERAL INFORMATION NO. USZUUJJUJJJJJJJAL

APPLICANT: Rockwell, Patricia
APPLICANT: Rockwell, Patricia
APPLICANT: GOLGAGEGIN, Noil I.
ITTLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689
FRIOR FILING DATE: 1999-09-22
PRIOR PELICATION NUMBER: 08/967,113
PRIOR FILING DATE: 1999-11-10
PRIOR PELICATION NUMBER: 08/706,804
PRIOR PELICATION NUMBER: 08/706,804
PRIOR PELICATION NUMBER: 08/326,522
PRIOR PELICATION NUMBER: 08/326,522
PRIOR PELICATION NUMBER: 08/326,633
PRIOR FILING DATE: 1994-10-20
PRIOR PELICATION NUMBER: 08/196,041
PRIOR PELICATION NUMBER: 08/196,041 ö o; Query Match 100.0%; Score 62; DB 10; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 11; Conservative 0; Mismatches 0; Indels .. 0

> .. 0

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Sequence 111, Application US/10374531

Sequence 111, Application US/10374531

Publication No. US20040006212A1

GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTERIOR OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 12; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
     REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPAK: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PELLING DATE: 25-Peb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-374-600-111
REGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                      LENGIH: 11 amino acids
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0
                                                                                             TELEFAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 111: SEQUENCE CHARACTERISTICS:
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ZIP: 10004
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                       Sequence 6, Application US/09996954B
; Sequence 6, Application US/09996954B
; Publication No. US20030157104A1
; GENERAL INFORMATION:
    APPLICANT: Waksal, Harlan W.
    TITLE OF INVENTION: Treatment of Refractory Human Tumors
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: WITHER: US/09/996,954B
    CURRENT FILING DATE: 2001-11-30
    FRIOR PELIOR NUMBER: 09/840,146
    PRIOR APPLICATION NUMBER: 09/312,284
    PRIOR FILING DATE: 08-14-1999
; PRIOR FILING DATE: 05-14-1999
; NUMBER OF SEQ ID NOS: 12
    SEQ ID NOS: 12
    SEQ ID NOS: 12
    SEQ ID NOS: 12
    TENGRALL: 11
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US-10-374-600-111
US-10-374-600-111, Application US/10374600
; Sequence 111, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: IMCIONE Systems Incorporated, et al.
; APPLICANT: IMCIONE Systems INCORPORATION:
TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 10; Length 11; 100.0%; Pred. No. 0.0015; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-MAT-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens-Rodent Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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     ALTYYDYEFAY 11
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ZIP: 10004
                                                                           RESULT 2
US-09-996-954B-6
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ublication No. Control of Systems Incorporated, et al.
APPLICANT: InClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS
INTEL OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/08/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/ABORT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 25-Feb-2003
FLING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDRESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRACHENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-374-531-99
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSES: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                      US-10-374-531-99; Sequence 99, Application US/10374531; Publication No. US20040006212A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: US
               2 ALTYYDYEFAY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ALTYYDYEFAY 12
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Publication No. US20030224001A1
GENERAL INCORMATION:
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTIBODY SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: LBM compatible COMPUTER: LBM compatible COMPUTER: LBM compatible COMPUTER: LBM compatible CURRENT APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION NUMBER: US/10/374,600 FILING DATE: 19-Mar-1998 APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998 APPLICATION NUMBER: US/08/482,982 FILING DATE: 07-JUN-1996 APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1996 APPLICATION NUMBER: US 08/482,982 FILING DATE: 15-DEC-1995 APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995 ATTORNEY/AGENT INFORMATION: NUMBER: US 08/573,289 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   Query Match
100.0%; Score 62; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 62; DB 12; Length 13; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INPORMATION:
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-10-374-531-111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 425-7200
TELEFAR: (212) 425-5288
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 13 amino acids
                                                                                                                                                                                                                                                       1 ALTYYDYEFAY 11
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US-10-374-600-115
US-10-374-600-115
; Sequence 115, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: ImClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
Query Match 100.0%; Score 62; DB 15; Length 13; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 11; Conservative 0; Mismatches 0; Indels
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1 ALTYYDYEFAY 11

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100.0%; Score 62; DB 12; Length 119; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10004
COMPUTER READBBLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPPEATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

RAPLICATION NUMBER: US/10/374,600
FILLING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Max-1998
APPLICATION NUMBER: PCT/US96/09847
                                                                                     PRIOR DATE: 25-Feb-2003

FILING DATE: 25-Feb-2003

CLASSIFICATION : CURROWN-
PRIOR APPLICATION NUMBER: US/08/973,065C

APPLICATION NUMBER: US/08/973,065C

FILING DATE: 19-Mar-1998

APPLICATION NUMBER: US/08/9847

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/482,982

FILING DATE: 10-MBER: US 08/482,982

FILING DATE: 15-DEC-1995

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPRAK: (212) 425-5286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
TYPE: amino acid
STARNDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117, Application US/10374600; Publication No. US20030224001A1 GENERAL INFORMATION:
COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
                                             SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 116: SEQUENCE CHARACTERISTICS:
                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALTYYDYEFAY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Y COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-374-600-117
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US-10-374-600-116
Sequence 116, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
INTEE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFER OF TOWORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
            INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:

NAME: Deborah A. Somerville
REGISTRATION UNDER: 31,995
REFERNCE/DOCKET UNMER: 31,995
REFERNCE/DOCKET UNMER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-MAR-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                       COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: Was Dos
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION CURROWD>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IBNGTH: 119 anino acids | TYDE: amino acids | TYDE: amino acid | STRANDEDNESS: not relevant | TOPOLOGY: not relevant | TOPOLOGY: not relevant | HYPOTHET TYPE: peptide | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 115: US-10-374-600-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
SIREET: One Broadway
CITY: New York
                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                           STREET: One Broadway
                                NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 ALTYYDYEFAY 108
                                                                                                                             CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALTYYDYEFAY 11
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 119, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: ZS-Feb-2003
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REJERRATION NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                              | JENUTH: 119 amino acids | TYPE: amino acids | TYPE: amino acid | STRANDEDNESS: not relevant | TOPOLOGY: not relevant | MOLECULE TYPE: peptide | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 118: US-10-374-600-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5286
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                  TELEFAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 118: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALTYYDYEFAY 11
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US-10-374-600-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US.10-374-600-118
US.10-374-600-118
Sequence 118, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
INTERIATION:
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible COMPUTER: US OF SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-MR-1998
APPLICATION NUMBER: US 08/973,065C
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAMM: Deborah A. Somerville
REGISTRATION NUMBER: 11,245/46003
FELEPRANCE/DOCKET NUMBER: 11245/46003
FELEPRANCE/DECHERISTICS:
BENGRIP: 119 amino acid
STRANDEDMES: not relevant
NOLECULE TYPE: amino acid
STRANDEDMES: not relevant
MOLECULE TYPE: peptide
HYPOTHERITCAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-374-600-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10004
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425-5288
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         STREET: One Broadway CITY: New York
                                                                                                                                       NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                              ZIP: 10004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 11, Conservative
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RESULT 13
US-10-374-531-115
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                               100.0%; Score 62; DB 12; Length 119; 100.0%; Pred. No. 0.016; ive 0; Mismatches 0; Indels (
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100.0%; Score 62; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                               APPLICANT: IMCIone Systems Incorporated, et al.
IITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847 FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-UW-1995
APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 120: US-10-374-600-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                           Sequence 120, Application US/10374600 Publication No. US20030224001A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425-5288
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INFORMATION FOR SEQ ID NO: 120:
SEQUENCE GRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10004
COMPUTER READABLE FORM:
                                   Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                          98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
                                                                                                        1 ALTYYDYEFAY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
 US-10-374-600-119
                                                                                                                                                                                           RESULT 12
US-10-374-600-120
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98 ALTYYDYEFAY 108

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Sequence 115. Application UN 191374531
Publication No. US200000212A1
Publication No. US2000000212A1
NUMBERS OF SEQUENCE ADDRESS 2
COMPERCED ADDRESS 3
COMPERCED AD
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Search completed: October 6, 2004, 17:09:03 Job time : 68.5088 secs
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US-10-374-531-117
Sequence 117, Application US/10374531
Publication No. US200040006212A1
GENERAL INFORMATION:
TILLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR THIRBITING THE GROWTH OF TUMORS
STREET: One block...,
CITY: New York
STATE: New York
COUNTRY: US
ZIATE: New York
COUNTRY: US
ZIATE: 10004
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
CORPUTER: IBM comparible
OPERATION TYPE: Diskette 3.5 inch 1.44 Mb storage
CORPUTER: IBM comparible
OPERATION TYPE: Diskette 3.5 inch 1.44 Mb storage
CORPUTER: IBM comparible
OPERATION TYPE: Diskette 3.5 inch 1.44 Mb storage
SOFTWARE: Wordperfect
CURRENT APPLICATION NUMBER: US/08/973,065C
FILING DATE: 25-Feb-2003
APPLICATION NUMBER: US/08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: 11245/46003
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 15; Length 119; 100.0%; Pred. No. 0.016;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Broadway CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-374-531-116
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Gaps
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FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Debortah A. SOMETVILLE
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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OM protein - protein search, using sw model

Run on: October 6, 2004, 16:24:54 ; Search time 19.4912 Seconds
(without alignments)
29.135 Million cell updates/sec
Title: US-09-635-974A-6
Sequence: 1 ALTYYDYEFAY 11

Perfect score: 62
Sequence: 1 ALTYYDYEFAY 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0%
Maximum'Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:*
1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query	ery		4	;			
Match I		Length	DB	QI	Description	r.	
		119	7	00-19	Seguence	2	Appli
62.9		119	m	-09-296-5	Sequence		Appli
•		240	7	-08-800-198-	Sequence	œ	Appli
N		240	ო	-296-59	Sequence	8	Appli
•		509	m	US-08-369-822C-26	Sequence	26,	Appl
		509	m	US-08-582-776C-41	Sequence	41,	Appl
61.3		509	m	US-08-434-831B-38	Sequence	38,	Appl
59.7		13	N	US-08-737-085A-2	Sequence	7	Appli
59.7		13	m	US-09-246-258-2	Sequence	7	Appli
59.7		13	m	US-09-532-106-2	Seguence	2	Appli
59.7		13	4	US-09-839-666-2	Sequence	7	Appli
59.7		14	Ŋ	συ	Sequence		Appli
59.7		14	m	US-09-246-258-1	Sequence	H	Appli
59.7		14	m	09-532-10	Sequence	ř	Appli
59.7		14	4	vo	Sequence	7	Appli
59.7		22	7	08-737-0	Sequence	13	Appl
59.7		22	m	09-246-2	Sequence		Appl
59.7		22	М	US-09-532-106-13	Sequence		App1
59.7		22	4,	US-09-839-666-13	Sequence	13,	Appl
ģ.		24	7	08-737-	Sequence		Appl
59.7		24	0	-08-737-	Sequence		Appl
59.7			~	08-737-08	Sequence	18	Appl
59.7			7	US-08-737-085A-23	Sequence	23,	Appl
59.7			ო	US-09-246-258-14	Sequence	14,	App1
59.7		24	m	-09-246-25	Sequence	17,	Appl
59.7			m	-09-246-2	Sequence	18,	Appl
59.7		24	m	US-09-246-258-23	Sequence	23,	Appl

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Query Match 62.9%; Score 39; DB 2; Length 119; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 1; Mismatches 1; Indels

Appl Appl Appl Appl Appl Appl Appl Appl
144, 100, 100, 100, 100, 100, 100, 100,
Sequence seq
US-09-532-106-14 US-09-532-106-18 US-09-532-106-18 US-09-839-666-14 US-09-839-666-17 US-09-839-666-18 US-09-839-666-19 US-09-839-666-19 US-09-839-666-19 US-09-532-106-19 US-09-532-106-19 US-08-737-085A-15 US-09-532-106-15 US-09-532-106-15 US-09-532-106-15 US-09-532-106-15 US-09-532-106-15
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US-08-800-198-2

US-08-800-198-2

Sequence 2, Application US/08800198

PALET NO. 5942602

GENERAL INFORMATION:

APPLICANT: WELS, WINFRIED S.

APPLICANT: SCHMIDT, MATHIAG.

CORRESPONDENCE MILLEN, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD. SUITE 1400

CITY: ARLINGTON

CONPUTER: US

CONPUTER: US

COMPUTER: ISM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: ISM PC Compatible

COMPUTER: ISM PC Compatible

COMPUTER: ISM PC Compatible

COMPUTER: ISM PC COMPANION:

MADIUM TYPE: ATTION DATE: 13-FEB-1997

CURSSIFICATION: 530

ATTORNEY, ACGENT INFORMATION:

MAME: HAMLET-KING, DIANA

REFERENCE/DOCKET NUMBER: SCH 1576

TELEPONE: 703-243-6410

TELEPONE: 703-243-6410

TELEPONE: 119 amino acide

TOPOLOGY: 11near

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ANTI-SENSE: NO

ANTI-SENSE: NO

MATHIAGENERAL TYPE: internal
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Sequence 26, Application US/0836982C

Sequence 26, Application US/0836982C

Sequence 26, Application US/0836982C

GENERAL INFORMATION:
APPLICANT: Briese, Thomas
APPLICANT: Schneider, Parrick A.
APPL
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 25;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WINFRIED S.
APPLICANT: SCHMIDT, WINFRIED S.
APPLICANT: SCHMIDT, WATHIAS
APPLICANT: SCHMIDT, WATHIAS
APPLICANT: SCHMIDT, WATHIAS
APPLICANT: SCHWIDTER, DOUGLE, EVANGELIA.
APPLICANT: SCHWIDTER, DOUGLES
TITLE REFERENCE: SCH-1576 D1
CURRENT APPLICATION NUMBER: US/09/296,595A
CURRENT FILING DATE: 1999-04-23
BARLIER APPLICATION NUMBER: 08/800,198
BARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Fulbright & Jaworski, L.L.P.
865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 3;
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09296595A Patent No. 6129915 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.9%;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
LENGTH: 240 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                  internal
                                                                                                                                 MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90017-2571
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 YYGYDFAY 108
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                                                                                                         linear
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ORGANISM: Murine sp.
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                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                             US-08-800-198-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-296-595-8
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Pred. No. 12;
1; Mismatches 1; Indels
                                                                                                                                                                                                                   Sequence 2, Application US/09296595A

Sequence 2, Application US/09296595A

Patent No. 6129915

GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATHIAS
APPLICANT: SCHMIDT, MATHIAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
TITLE OF INVENTION: GROWTH FACTOR
FILE REFERENCE: SCH-1576 D1
CURRENT APPLICATION NUMBER: US/09/296,595A
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 08/800,198
BARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver: 2.1
FENDING 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08800198
Patent No. 5942862
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATHIAS
APPLICANT: SCHMIDT, MATHIAS
APPLICANT: SCHNIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIP: 22201
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATOR DELICATION PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILLING DATE: 13-FEB-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPERENCE/DOCKET NUMBER: 33,302
REPERENCE/DOCKET NUMBER: SCH
TELECOMUNICATION INFORMATION:
TELEPHONE: 703.243-6333
TELEPAX: 703.243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 YYGYDFAY 108
                                                                       101 YYGYDFAY 108
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                 YYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Murine sp.
US-09-296-595-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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Gaps

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US-08-434-831B-38
Sequence 39, Application US/08434831B
Sequence 39, Application US/08434831B
Sequence No. 6113905
SEPLICANT Lipkin, W. I.
APPLICANT Lipkin, W. I.
APPLICANT SCHLEGET, Farrick A.
APPLICANT SCHLEGET, Parrick A.
APPLICANT SCHLEGET, SCHEMEN Disease Viral Sequences,
ITILE OF INVENTION: Disagnostics and Therapeutics for Central Nervous
ITILE OF INVENTION: Disagnostics and Therapeutics for Central Nervous
ITILE OF INVENTION: System Disease
CONTRY: California
CONTRY: California
CONTRY: California
CONTRY: Test Flory disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flory MINDOMS NT-WCRDFERFECT 8.0
SOFTWARE: ASLONALE FORM:
MEDIUM TYPE: APPLICANTON NATA:
COMPUTER: APPLICANTON NATA:
COMPUTER: APPLICANTON AND ATA:
APPLICANTON NUMBER: US/08/434,831B
CLASSIFICANTION HOWER: US/08/434,831B
FILING DATE: OF-ANAL195
ATTONEY APPLICANTON HOWER: SHEEL OF THE STANDAL STANDAL SHEEL SHEEL OF THE STANDAL SHEEL SHE
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Pred. No. 81;
2; Mismatches 1; Indels
                                                       1279-194C2
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279
TELECOMMUNICATION INFORMATION:
TELEPAX: 213/682-9200
TELEPAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 anino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 509 amino acide TYPE: amino acide TOPOLOY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 TYFDSEFSY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ANTI-SENSE: NO
US-08-582-776C-41
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APPLICANT: Briese, Thomas
APPLICANT: Briese, Thomas
APPLICANT: Strack, Stefanic
APPLICANT: Schneider, Patrick A.
APPLICANT: Stitz, Lothar
APPLICANT: Schneemann, Anette
APPLICANTION: System Disease Viral Sequences,
TITLE OF INVENTION: System Disease
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figuerca Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.3%; Score 38; DB 3; Length 509; 66.7%; Pred. No. 81; tive 2; Mismatches 1; Indels
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,82C
FILING DATE: 06-JAN-1995
CLASSIFICATION NUMBER: 39,944
REGISTRATION NUMBER: 39,944
REGISTRATION NUMBER: 1279-194XX
TELECOMUNICATION INFORMATION:
TELEPHONE: 213/892-9200
TELEPHONE: 213/892-9200
TELECOMUNICATION INFORMATION:
TELEPHONE: 213/892-9200
TELEPHONE: 213/892-9200
TELEPHONE: 213/892-9200
TELEPHONE: 213/892-9300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/08582776C Patent No. 6077510 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 TYFDSEFSY 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-369-822C-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-582-776C-41
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APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-532-106-2
; Sequence 2, Application US/09532106
; Patent No. 6245892
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-09-246-258-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LTYYDYEFAY 11
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                  CITY: Ne
STATE: N
COUNTRY:
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Matches
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                                                                      Gaps
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0
                             Score 38; DB 3; Length 509;
Pred. No. 81;
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                                                                    1; Indels
                                                                                                                                                                                                                       Sequence 2, Application US/08737085A
Fatent No. 586932
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09246258
Patent No. 6040137
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRIES

ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A

**TING DATE: 27-DEC-1996
                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3846/0C569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846,
TELECOMMUNICATION INFORMATION:
TELEFRONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
70.0%;
                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-DEC-1
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
LENGTH: 13 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                       446 TYFDSEFSY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIYYDYEEDY 12
                                                                                                    3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
JS-08-434-831B-38
                                                                                                                                                                                         RESULT 8
US-08-737-085A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-737-085A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-246-258-2
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY EXCHANGER
ZIP: 10022
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,258
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                              FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: DARBY & DARBY P
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
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Gaps
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0
                  Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                         Sequence 1, Application US/08737085A
Patent No. 5869232
GBNERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: EXCHANGER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESSES: DARBY PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09246258
Patent No. 6040137
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: EXCHANGER
TUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS

SOFTWARE: Fast SEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A

FILING DATE: 27-DEC-1996

CLASSIFICATION: 426

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Green, Reza

REGISTRATION NUMBER: 38,475

REGISTRATION NUMBER: 38,475
                Score 37; DB 4
Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 2
Pred. No. 2.6;
0; Mismatches
              59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
Query Match
Best Local Similarity 70.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                           2 LTYYDYEFAY 11
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                                                                                                                             LIYYDYEEDY
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New Yor!
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                                                                                                                                                                                                                                                                                                                                                           59.7%; Score 37; DB 3; Length 13; 70.0%; Pred. No. 2.4; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FastSEQ for Windows Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-Apr-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09839666
Patent No. 6469143
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: EXCHANGER
                            NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELERX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERRENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELER: 236687
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-532-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION WHOBER: 08/737,085
FILING DATE: «UNKnown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: DARBY & DARBY
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                     LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LIYYDYEEDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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US-09-839-666-2
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us-09-635-974a-6.rai

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Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%; Score 37; DB 3; 70.0%; Pred. No. 2.6;
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TELECOMMUNICATION: INPORMATION:
TELEBENONE: 212-227-7659
TELEBEAX: 212-753-6237
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/9/839,666
FILING DATE: 19-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
MAME: Green, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0, Mismatches
                                                                                                                                                                                                                                     TOPOLOGY: linear

NOLECTLE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-839-666-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 Third Avenue
                                                                            TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236697
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09839666
Patent No. 6469143
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
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Best Local Similarity
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Pred. No. 2.6;
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Patent No. 6245895
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
ATTLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21.Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
COMPUTER: 1BM COMPATIBLE
CORRATING SYSTEM: DOS
SOFTWARE: FASTERE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NIMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA;
PRIOR APPLICATION NUMBER: 08/737,085
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELEPHONE: 212-527-7559
TELEPHONE: 212-537-7559
TELEPHONE: 212-537-7559
TELEPHONE: 212-537-7559
TELEPHONE: 212-537-7559
TELEPHONE: 212-537-7559
TELEPHONE: 216-733-6237
TELEPHONE: 216-733-6237
TELEPHONE: 216-733-6237
TELEFR: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
   ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
CIIY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70...
7, Conservative
                                                                                                                 COUNTRY: USA
CONTUTER 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-246-258-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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0; Gaps 3; Indels 0; Mismatches 7; Conservative 2 LTYYDYEFAY 11 | | | | | | | | | | | | 3 LIYYDYEEDY 12 Matches දු දු

Search completed: October 6, 2004, 16:36:32 Job time: 20.4912 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

October 6, 2004, 16:20:48; Search time 55.5789 Seconds (without alignments) 55.921 Million cell updates/sec Run on:

US-09-635-974A-6 62 Perfect score: Title:

1 ALTYYDYEFAY 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: qeneseqp1980s:* Database :

geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* geneseqp1980s;* geneseqp1990s;* geneseqp2004s: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aay59313 Heavy cha	54	86	3 Heavy	50 Heavy	52 Heavy	951 Heavy	4 Heavy		4 Heavy	2 Heavy	Ψ		Aaw05140 scFv2(225	σ		Abg10386 Novel hum		Aab19756 Erythropo	Aay56681 Anti-eryt	22	5	Aab19745 Erythropo	8	Aab19747 Erythropo
DI	AAY59313	AAB37954	AAU77786	AAW08953	AAW08950	AAW08952	AAW08951	AAW08954	AAW08947	AAW08944	AAW08942	AAW05133	AAW05135	AAW05140	AAW05139	AAW05141	ABG10386	ABP28261	AAB19756	AAY56681	AAY56682	AAY56705	AAB19745	AAB19748	AAB19747
Length DB		н	_	19	19	19	61	19	38	38	138 2	40	51	92	92	50	m	10	0	18	o.	20	20	LO.	ın.
% Query Match I	1.00.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	67.7	66.1	64.5	64.5	64.5	64.5	64.5	64.5	64.5
Score	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	42	41	40	40	40	40	40	40	40
Result No.	-	7	m	4	w	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20			23		25

Aaw71240 Heavy cha	Aaw71243 scFv comp	Aar13721 Control £		-	Abp75850 Human sec	_	Aar84527 CDRH3 of	Aar84526 CDRH3 of	Aaw38244 CDR3-H3 s	Aar84538 Anti-HIV-	Aar84539 Anti-HIV-	Aar84543 Anti-HIV-	Aar84548 Anti-HIV-		Aar84544 2[Anti-HI	Aar84540 Anti-HIV-	Aar84541 Anti-HIV-	Abg03953 Novel hum	
AAW71240	: AAW71243	: AAR13721	ABM74082	, ABM73723	3 ABP75850	ADB64342	: AAR84527	: AAR84526	: AAW38244	AAR84538	. AAR84539			AAR84542	. AAR84544	AAR84540	AAR84541	ABG03953	AAR48619
119 2	240 2	120 2	322 7	471 7	561 6	815 7	13 2	14 2	14 2	22 2	24 2	4,	24 2	24 2	'n	26 2	26 2	115 4	120 2
9 62.9	9 62.9	5 62.1	9 61.3	9 61.3	3 61.3	3 61.3	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7	7 59.7
26 3:	27 3	28 38.5	29 3	30 36	31 3	32 3	33 3.	34 3.	35 3.	36 3.	37 3.	38 3	. 39	40 3.	41 3.	42 3.	43 3.	44 3.	45 37

# ALIGNMENTS

Hypervariable region; complementarity determining region; CDR; tumour; single chain antibody; growth inhibitor; human; tumourigenesis; therapy; protein receptor tyrosine kinase; heavy chain. Heavy chain hypervariable region, CDR3. AAY59313 standard; peptide; 11 AA 07-MAR-2000 (first entry) AAY59313; AAY59313 

Mus sp.

WO9960023-A1.

25-NOV-1999.

98US-00079612. 98US-0085613P. 98US-00206138. 99WO-US010741. 15-MAY-1998; 15-MAY-1998; 07-DEC-1998; 14-MAY-1999;

(IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND.

Robert F, Buchsbaum DJ; Waksal HW, Saleh MN,

WPI; 2000-062440/05. N-PSDB; AAZ48627.

Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.

Disclosure, Page 15; 31pp; English.

This sequence is the hypervariable region CDR3 (complementarity determining region 3) of the heavy chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by traating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumoursigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to

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1 ALTYYDYEFAY 11

(first entry)

SXS

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Mouse heavy chain hypervariable region (CDR3) of 225 antibody
                                                                                                                                     AAU77786 standard; peptide; 11
                                                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                  AAU77786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                           RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a method for inhibiting the growth of refractory tumours that are stimulated by a ligand of epidermal growth factor receptor (BGFR) in human patients. The method involves treating the patient with a combination of BGFR/human EGF-1 (HER1) antagonist, optionally with a chemctherapeutic agent or radiation. The antagonist can BGFR/HRR1 artagonist anti-EGFR monoclonal antibody, C225. The BGFR/HRR1 is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, spine, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence region 3 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-EGFR monoclonal antibody H chain V region CDR3 peptide sequence.
                                                                                                                                          Gaps
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the patient makes the tumour more susceptible to radiotherapy
                                                                                           Length 11;
                                                                                                                                     0; Indels
                                                                                           100.0%; Score 62; DB 3; I
100.0%; Pred. No. 0.00041;
                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                     AAB37954 standard; protein; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2001 (first entry)
                                                                                                               Local Similarity 100 es 11; Conservative
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                                                                                                                                                                                                                  WPI; 2001-016160/02.
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                                                 Sequence 11 AA;
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                                                                                              Query Match
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AAB37964

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AAB379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
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Mouse; heavy chain; antibody; hyperproliferative disease; epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR3; EGFR inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 12; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2000; 2000US-00635974.
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AAW08953
ID AAW0
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ch 100.0%; Score 62; DB 4; Length 11; Similarity 100.0%; Pred. No. 0.00041; 11; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 11, Conservat

1 ALTYYDYEFAY 11

Campung CDR-7

Heavy chain; reshaped; monoclonal; antibody; 225RA; human; eppldarmal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostatic variable region; framework; complementarity determining region; CDF

Location/Qualifiers . .30 label= framework_l

Homo sapiens

Key Region Region Region Region Region Region Region

36. .49 /label= framework_2 50. .65 /label= CDR_2 66. .97 /label= framework_3

CDR_1

1. .35 label=

WO9640210-A1

CDR_3

/label=

.108

Heavy chain variable region of 225RA antibody.

(first entry)

18-SEP-1997

AAW08950;

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Heavy chain; reshaped; monoclonal; antibody; 225RD; human; pepidermal growth factor; BGR; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H325, 225RHO. The MAb is specific for the human motoclonal antibody (MAb) H325, 255RHO. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage by posteatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
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                                               Heavy chain variable region of 225RD antibody.
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                                                                                                                                                                                            31. .35
/label= CDR_1
36. .49
/label= framework_2
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/label= CDR_2
66. .97
/label= framework_3
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109. .119
/label= framework_4
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/label= framework_1
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                         (first entry)
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                                                                                                                                  Homo sapiens
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15-DEC-1995;
                      18-SEP-1997
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(MRCC-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
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100.0%; Score 62; DB 2; Length 119; llarity 100.0%; Pred. No. 0.0056; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 11; Conserv

RESULT 5 AAW08950 ID AAW08950 standard; protein; 119 AA. XX

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1 ALTYYDYEFAY

Saldanha JW;

Giorgio NA, Jones ST,

WPI; 1997-051897/05.

Goldstein NI,

(IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.

07-JUN-1995; 15-DEC-1995;

96WO-US009847 95US-00482982 95US-00573289

07-JUN-1996; 19-DEC-1996.

tumour; cell;

AAW08952,

Key Region Region Region Region Region Region Region

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The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHB. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                    Heavy chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
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100.0%; Pred. No. 0.0056;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha JW;
                                                           Heavy chain variable region of 225RB antibody.
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label= framework_1
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/label= framework_2
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/label= framework_4
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label= CDR_1
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/label= CDR_2
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/label= CDR_3
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15-DEC-1995;
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                                                                                           Heavy chain; reshaped; monoclonal; antibody; 225RC; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW;
                                                                variable region of 225RC antibody.
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                                                                                                                                                                                                                                                                                                                                                       56. .97 __/label= framework_3
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label= framework_2
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/label= framework_4
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label= framework 1
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/label= CDR_3
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/label= CDR_1
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/label= CDR_2
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Best Local Similarity
Matches 11, Conserv
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                                                                                                                                                                               Homo sapiens
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15-DEC-1995;
                                     18-SEP-1997
                                                                 Heavy chain
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AAW08954 standard; protein; 119 AA.

AAW08954 ID AAWC XX

AAW08951 ID AAW08951 standard, protein, 119 AA. XX

RESULT 7

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(first entry)

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Heavy chain; reshaped; monoclonal; antibody; 225RA; human;
epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell;
late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                     Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                 Heavy chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                    Claim 31; Fig 20; 112pp; English.
                                                                                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT
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N-PSDB; AAT49346.
                                                                                                                                                                                                                                                                             Goldstein NI,
                                                                                                                    Homo sapiens
                                                                                                                                        WO9640210-A1
                                                                                                                                                                                     07-JUN-1996;
                          18-SEP-1997
                                                                                                                                                                                                         07-JUN-1995;
15-DEC-1995;
                                                                                                                                                              19-DEC-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-1997
    AAW08947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW08944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
AAW08944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                            epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHE. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and humanised versions of anti-EGF receptor antibody 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of late stage prostatic tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 2; Length 119; 100.0%; Pred. No. 0.0056; Pred. No. 0.0056; ive 0; Mismatches 0; Indels
                                                                   reshaped; monoclonal; antibody; 225RE; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giorgio NA, Jones ST, Saldanha JW;
                                           Heavy chain variable region of 225RE antibody.
                                                                                                                                                                                                                           50. .65
/label= CDR_2
66. .97
/label= framework_3
                                                                                                                                                          1. 30
/label= framework_1
31. 35
/label= CDR_1
36. 49
/label= framework_2
                                                                                                                                                                                                                                                                       98 ...08
/label= CDR 3
109. .119
/label= framework_4
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibiting tumour growth, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                  95US-00482982
95US-00573289
                                                                                                                                                                                                                                                                                                                                                                             96WO-US009847
                     18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
And 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-051897/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldstein NI,
                                                                Heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996
 AAW08954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                          Region
                                                                                                                                                                                 Region
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                                                                                                                                                 Key
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- nsed

Giorgio NA, Jones ST, Saldanha JW;

96WO-US009847. 95US-00482982 95US-00573289

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The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H255, 225RHA. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tunnour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain, murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                         100.0%; Score 62; DB 2; Length 138; 100.0%; Pred. No. 0.0065; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain variable region of C225 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW08944 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                            Best Local Similarity 100
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                            117 ALTYYDYEFAY 127
                                                                                                                                                                                                                                                                                           1 ALTYYDYEFAY 11
                                                                                                                                                                  Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus; spp.
Homo sapiens.
Synthetic.
Chimeric.
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Gaps

0;

RESULT 9
AAW08947
ID AAW08947 standard, protein; 138 AA.
XX

ALTYYDYEFAY 108 1 ALTYYDYEFAY 11

86

ò d ö

Gaps ..

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The present sequence is the heavy chain variable region of the murine monoclonal antibody (MAD) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to timbibt the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AVG-2003 to correct OS field.)
           Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single chain antibody; scFv; monoclonal antibody; MAD; EGF; epidermal growth factor; receptor; antitumour; cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /noce= "synthetic spacer peptide"
| 134. 240
| 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 158 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .119
/label= VH_region
/note= "monoclonal antibody 225 VH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW05133 standard; protein; 240 AA.
                                                                                                     Example IV; Fig 14; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 17; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single chain antibody scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120. .133
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 ALTYYDYEFAY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-478748/48.
N-PSDB; AAT42033.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus; sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW05133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW0513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the heavy chain variable region of the chimeric monoclonal antibody (MAD) C225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, rass or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain; murine; mouse; monoclonal; antibody; M225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                 Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable region of M225 antibody.
                                                                                                                                                                                                                                                                                                                    Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example IV; Fig 16; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW08942 standard; protein; 138 AA.
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                                                                                                                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT
                                                                                      96WO-US009847.
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95US-00573289
                                                                                                                                               95US-00482982
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 ALTYYDYEFAY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALTYYDYEFAY 11
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N-PSDB; AAT49340.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT49343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain;
epidermal gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1996;
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15-DEC-1995;
                                                                                         07-JUN-1996;
                                                                                                                                               07-JUN-1995;
15-DEC-1995;
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18-SEP-1997
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                                   19-DEC-1996
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AAW08942;

RESULT 11

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Gaps ö

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scFv(225) (AAW05133) comprises the single-chain binding region of murine monoclonal antibody 225, which is specific for the human epidermal growth factor receptor. It is encoded by plasmid pWW152-225 (see also AAT42033), constructed by cloning MAD 225 will and VI region cDNAs into plasmid pWW152. Novel bivalent proteins (see also AAW05134-44), some of them including scFv(225) and an effector e.g. cytotoxin, can be produced in bacterial host cells, and are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                          Single chain antibody, scPv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; plasmid pSW202-225; cancer; therapy; antitumour; exotoxin A; ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                    Query Match 100.0%; Score 62; DB 2; Length 240; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290. .651
/label= ETA
/note= "exotoxin A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .21
/label= Sig_peptide
/note= "ompA signal p
                                                                                                                                                                                                                                                                           AAW05135 standard; protein; 651 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                 scFv(225)-ETA fusion protein.
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                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                      ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
Pseudomonas, aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                      1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-478748/48.
N-PSDB; AAT42035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt M,
                                                                                                               Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1995;
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Peptide
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X88888888888888
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Example 7; Page 19-20; 52pp; English.

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        scFv(225)-ETA (AAW05135) comprises the single-chain binding region (see also AAW05133) of murine monoclonal antibody 225, which is specific for human epidermal growth factor receptor, joined to exotoxin A (ETA). It is encoded by plasmid pSW202-225 (see also AAT42035) obtd. by ligating an scFv(225) gene (AAY42033) into plasmid pSW200 contg. the Pseudomonas acruginosa PAK ETA gene. The construct can be used to produce novel bivalent fusion proteins (see also AAW05136-44) in bacterial host cells, for use as antitumour agents
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                    Single chain antibody; scFv; monoclonal antibody; NAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-225-5; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                                  ..
0
                                                                                                                                        100.0%; Score 62; DB 2; Length 651; 100.0%; Pred. No. 0.036; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648. .658
/label= Spacer
659. .892
/label= ETA
/note= "endotoxin-A amino acids 380-613"
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/label= ETA
/note= "exotoxin A amino acids 252-366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . 21
/label= Sig_peptide
/note= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                        AAW05140 standard; protein; 892 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39. 278
/label= scrv(225)
279. 289
/label= Spacer
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:08. .647
|label= scFv(FRP5)
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/label= Spacer
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                                                                                                                                                                                                                                                                                                                       29-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405. .407
/label= Sp
                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                            136 ALTYYDYEFAY 146
                                                                                                                                                                                         1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                            scrv2 (225/FRP5) -ETA.
                                                                                                                  Sequence 651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1996.
                                                                                                                                                                                                                                                                                               AAW05140;
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Peptide
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AAW05140
X8888888888X8
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26-APR-1995;
                                                                      26-APR-1995;
         EP739984-A1
                             30-0CT-1996.
                                                                                                              Wels W,
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Job time :
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                                                                                                          scFv2(225/FRP5)-ETA (AAW05140) comprises the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW0513) Joined to portions of exocorin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor erbB-2, see also AAW05134). It is encoded by plasmid pMS238-225-5 (AAT42040). This plasmid can be utilised in the prodn. of the bivalent protein in bacterial (sep. B. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                 Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-5-225; cancer; exotoxin A; ETA; antitumour.
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0
                                                                                                                                                                                                                                       Query Match 100.0%; Score 62; DB 2; Length 892; Best Local Similarity 100.0%; Pred. No. 0.051; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "endotoxin-A amino acids 380-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "exotoxin A amino acids 252-366"
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/label= Sig peptide
/note= "ompA signal peptide"
                                                                                           Example 11; Page 31-33; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                         AAW05139 standard; protein; 892 AA
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/label= Spacer
39. .278
/label= scFv(FRI
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/label= Spacer
659. .892
/label= ETA
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/label= ETA
  Groner
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/label= Sr
90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas; aeruginosa.
Synthetic
                                                                                                                                                                                                                                                                                  1 ALTYYDYEFAY 11
                    WPI; 1996-478748/48.
N-PSDB; AAT42040.
Schmidt M,
                                                                                                                                                                                                                     Sequence 892 AA;
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Peptide
  Wels W,
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of murine monoclonal antibody FRP5 (specific for human epidermal growth actor receptor erbB-2, see also AAW05134) joined to portions of exotoxin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW05133). It is encoded by plasmid pMS228-5-225 (AAT42039). This plasmid can be utilised in the prodn of the bivalent fusion protein in bacterial (sep. E. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                    Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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100.0%; Pred. No. 0.051;
ive 0; Mismatches 0; Indels
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Ne : 57.5789 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page 28-30; 52pp; English.
                                                                                                                                  SANT-) SAN TUMORFORSCHUNGS GMBH.
95EP-00106275.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                            WPI; 1996-478748/48.
                                                                                                                                                                                                                                                                                                         N-PSDB; AAT42039.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

224 12. 22. 12 12. 12. 12.

October 6, 2004, 16:34:15; Search time 68.5088 Seconds (without alignments) 51.669 Million cell updates/sec OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-635-974A-8 55 1. RASQSIGTNIH 11 Title: Perfect score: Scoring table: Sequence: Run on:

1351062 Total number of hits satisfying chosen parameters: 1351062 seqs, 321799191 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	* Query Match	* Query Match Length DB	DB	ΩI	Description	
-	552	100.0	11	10	US-09-798-689-32	Sequence 32	32, Ap
2	55	100.0	11	10	US-09-996-954B-8	Sequence 8	3, App
m	55	100.0	11	12	US-10-374-600-100	Sequence 1	1001
4	55	100.0	11	15	US-10-374-531-100	Seguence 1	100, A
Ŋ	55	100.0	107	σ	US-09-991-470-25	Sequence 25,	5, App
9	55	100.0	107	12	US-10-374-600-113	Seguence 1	
7	55	100.0	107	12	US-10-374-600-114	Sequence 1	114, 2
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σ.	55	100.0	107	15	US-10-374-531-114	Sequence 1	114, 7
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12	55	100.0	127	12	US-10-374-600-11	Sequence 1	11, Ap
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14	S	100.0	127	12	US-10-374-600-17	Sequence 1	17, Ag
15	55	100.0	127	15	US-10-374-531-5	Sequence 5	5, App

equence 11  quence 21  quence 22  quence 23  equence 24  equence 33  equence 33  equence 33  equence 23	Sequence 38, Appl
US-10-374-531-11 US-10-374-531-11 US-10-374-531-11 US-10-374-531-11 US-10-374-531-11 US-10-453-656-31 US-10-453-656-31 US-10-453-698-11 US-10-453-698-11 US-10-308-817-11	12 US-10-453-698-38
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### ALIGNMENTS

APPLICANT: Rockwell, Patricia
APPLICANT: Rockwell, Neil I.
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Genthod for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Method for Reducing and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT PELLING DATE: 2001-03-403
PRIOR PELLING DATE: 1999-09-22
PRIOR PELLING DATE: 1999-09-3
PRIOR PELLING DATE: 1995-09-03
PRIOR PELLING DATE: 1996-09-03
PRIOR PELLING DATE: 1996-09-03
PRIOR PELLING DATE: 1994-10-20
PRIOR PELLING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver: 2.1 .. 0 Gaps .. 0 Query Match 100.0%; Score 55; DB 10; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00059; Matches 11; Conservative 0; Mismatches 0; Indels Sequence 32, Application US/09798689; Publication No. US20030103973A1; GENERAL INFORMATION: , ORGANISM: Mouse US-09-798-689-32

1 RASQSIGTNIH 11 à

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Gaps
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US-10-374-531-100
; Sequence 100, Application US/10374531
; Publication No. US20040006212A1
; GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1,44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 55; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 11; Conservative 0; Mismatches 0;
                      REFERENCE/DOCKET NUMBER: 11245/46003 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998 APPLICATION NUMBER: PCT/US96/09847 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERRENCE/DOCKET NUMBER: 11245/46003
TELEPRONE: (212) 425-7200
TELEPRONE: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible
CORFUTER: Wordperfect
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: 25-Feb-2003
CIASSIFCATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                               TYPE: amino acid

TYPE: amino acid

STRANDEDNES: not relevant
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-374-600-100
REGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                   TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     LENGIH: 11 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASQSIGTNIH 11
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                                                                                                    Sequence 8. Application US/0996954B

Publication No. US20030157104A1

GENERAL INFORMATION:

APPLICANT: Maksal, Harlan W.

TITLE OF INVENTION: Treatment of Refractory Human Tumors

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: WITHER: US/09/996,954B

CURRENT FILING DATE: 201-11-30

FRIOR FILING DATE: 04-24-2001

FRIOR FILING DATE: 06-13-1999

PRIOR FILING DATE: 06-13-1999

NUMBER OF SEQ ID NOS: 12

SEQ ID NOS: 12
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US-10-374-600-100
is Sequence 100, Application US/10374600
is Publication No. US20030224001A1
is GENERAL INFORMATION: ANTIBODY AND ANTIBODY FRAGMENTS FOR TITLE OF INVENTION:

TITLE OF INVENTION:

1.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 10; Length 11; 100.0%; Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
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FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/ACENT INFORMATION:
NAME: Deborah A. SOMETVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens-Rodent Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASOSIGTNIH 11
  1 RASQSIGTNIH 11
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Best Local Similarity
Matches 11; Conserv
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASQSIGTNIH 11
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Sequence 25, Application US/09991470

GENERAL INFORMATION:

APPLICANT: Ruey S. Liou

TITLE OF INVENTYON: ANTI-IGE GENE THERAPY
FILE REPRENCE: 99-201-11-20

CURRENT APPLICATION UNBER: US/09/991,470

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION UNBER: EARLIER APPLICATION NUMBER: 09/397,569

PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 107
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Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 9; Length 107; 100.0%; Pred. No. 0.0065; ive 0; Mismatches 0; Indels
                                                                                                                                    Length 11;
                                                                                                                                                                            Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                  Query Match

Dest Local Similarity 100.0%; Pred. No. 0.00059;

Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-MAI-1998
APPLICATION NUMBER: PCT/US96/09847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
PILING DATE: 25-Feb-2003
CLASSIFICATION: «URMOWN»
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-10-374-531-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RASQSIGTNIH 11
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                                                                                                                                                                                                                                                             1 RASQSIGTNIH 11
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CRGANISM: human/murine
US-09-991-470-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-374-600-113
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Gaps . Length 107; Sequence 114, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
ATILE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION: INHIBITING THE GROWTH OF TUMORS COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible COMPUTER: IBM compatible COMPUTER: IBM compatible COMPUTER: IBM compatible COMPUTER: Wardperfect CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1996
APPLICATION NUMBER: CT/US96/0987
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995 Indels Query Match
100.0%; Score 55; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995

ATTORNEY/ACBNT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995

REFERENCE/DOCKET NUMBER: 11245/46003

TELECOMUNICATION INFORMATION:
TELECHONE: (212) 425-7200

TELEPHONE: (212) 425-5288

INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid ATTORNEY/AGENT INFORMATION:
NAME: Deborar A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:

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(2-10-374-531-114
) Sequence 114, Application US/10374531
) Publication No. US20040006212A1
) Publication No. US20040006512A1
) GENERAL INFORMATION:

APPLICANT: Inclone Systems Incorporated, et al.

TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTELLING THE GROWTH OF TUMORS
                                                             100.0%; Score 55; DB 15; Length 107; 100.0%; Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55, DB 15; Length 107; 100.0%; Pred. No. 0.0065; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERRENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
                                                                                                           Mismatches
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APPLICATION NUMBER: US/10/374,531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
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Best Local Similarity
Matches 11; Conserv
          US-10-374-531-113
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2.10-374-531-113
9.210-374-531-113
9.20040006212A1
9. Publication No. US20040006212A1
9. Publication No. US20040006212A1
9. GENERAL INFORMATION:
7. APPLICANT: Imclone Systems Incorporated, et al.
9. APPLICANT: Imclone Systems Incorporated, et al.
9. TITLE OF INVENTION: ANTIBODY AND ANTIBODY PRAGMENTS
9. TITLE OF INVENTION: ANTIBOTY AND ANTIBODY PRAGMENTS
9. TITLE OF INVENTION: ANTIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 55; DB'12; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIPICATION CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US86/09847
FILING DATE: 07-UNN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UNN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid STRANDEDNESS: not relevant
FOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-374-600-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 113:
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US-10-374-600-11

| Sequence 11, Application US/10374600
| Publication No. US20030224001A1
| Publication No. US20030224001A1
| GENERAL INPORMATION:
| TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR TITLE OF INVENTION: ANTIBODY AND ANTIBODY PRAGMENTS FOR STREEP OF SEQUENCES: 120
| CORRESPONDENCE ADDRESS: Antiboral Correspondence Renyon STREET: One Broadway CITY: New York STATE: New York STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 12; 100.0%; Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION TO SUBMINANT PRIOR APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UW-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-374-600-11
                                                                                                                                                                                                                                       FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-10-374-600-5
                                                                                            STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10004
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 11; Conservative
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               ASSULPTION OF USCOLOUR AND APPLICATION NUMBER: 05/371,683

FURENZAL INFORMATION:
GENERAL INFORMATION:
FULL OF INVENTION: Recombinant Anti-Interleukin-9 Antibodies
FILE PEPERSNCE: IL4000C
GURRENT FILING DATE: 2003-04-11
FRICR APPLICATION NUMBER: 60/371,728
FRICR APPLICATION NUMBER: 60/371,728
FRICR APPLICATION NUMBER: 60/371,683
FRICR FILING DATE: 2002-04-12
FRICR 
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100.0%; Score 55; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT:/ImClone Systems Incorporated, et al.
ATITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New YORK
COUNTY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-412-703A-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 129
LENGTH: 108
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STATE: New York
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                                                                                                                                                                                                   CITY: New York
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  Length 127;
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                                                                                                                                                                                                                                                 DDICGITON NO. CONTROL OF THE SYSTEMS INCORPORATED, ET AL.
APPLICANT: INCIONE SYSTEMS INCORPORATED TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA: US/10/374,600 FILING DATE: 25-Peb-2003 CLASSIFICATION: ~Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 55; DB 12; Similarity 100.0%; Pred. No. 0.0079; 11; Conservative 0; Mismatches 0;
Query Match 100.0%; Score 55; DB 12; Best Local Similarity 100.0%; Pred. No. 0.0079; Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMUNICATION INPORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-10-374-600-15
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 127 amino acids
    TYPE: amino acid
    STRANDEDNESS: not relevant
    TOPOLOGY: not relevant
    MOLECULE TYPE: peptide
    HYPOTHETICAL: NO
                                                                                                                                                                            RESULT 13'
US-10-374-600-15
; Sequence 15, Application US/10374600
; Publication No. US20030224001A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 425-5288 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                               1 RASOSIGINIH 11
                                                                                                                        44 RASOSIGTNIH 54
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Best Local Similarity
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RESULT 14 US-10-374-600-17

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Sequence 17, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
APPLICANT: Imclone Systems Incorporatedy FRAGMENTS
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                         ZIP: 10004'
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION - UNKnown>
PRIOR APPLICATION DATA:
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: CT/US96/09847
FILING DATE: 19-Mar-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon STREET: One Broadway
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JENGTH: 127 amino acids YPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                             NUMBER OF SEQUENCES: 120
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Best Local Similarity 100.
Matches 11; Conservative
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STATE: New York

COUNTRY: 1004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage

COMPUTER: IBM compatible

OMERATING SYSTEM: MS.DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION NUMBER: US/10/374,531

FILING DATE: 25-Feb-2003

CLASSITCATION: CURACOM:

APPLICATION NUMBER: US/86/993,065C

FILING DATE: 19-Mar.1998

APPLICATION NUMBER: US/86/993,065C

FILING DATE: 19-Mar.1998

APPLICATION NUMBER: US/86/993,289

APPLICATION NUMBER: US/86/993

APPLICATION NUMBER: US/86/893

APPLICATION NUMBER: 13,995

APPLICATION
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Search completed: October 6, 2004, 17:09:05 Job time : 70.5088 secs

44 RASQSIGINIH 54

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0; Gaps

Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 11; Conservative 0; Mismatches 0; Indels C

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Q7vvm0 bordetella Q93yg8 lycopersico O65833 lycopersico Q7ux08 rhodopirell

Q9u183 homo sapien Q9u82 homo sapien Q9hw5 pseudomonas Q89cll bradyrhizob Q8742 mus musculu Q9d749 mus musculu Q9d748 mus musculu Q9bh48 mus musculu Q8773 aspergillus Q85sw6 mus musculu Q876i6 saccharomyc Q876i6 saccharomyc Q876i6 saccharomyc Q876i6 caenorhabdi Q720 bacteriopha Q91711 caenorhabdi Q91711 caenorhabdi

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q925S9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque:
01-OCT-2003 (TrEMBLrel. 25, Last annot.
Immunoglobulin light chain (Fragment).
Mus musculus (Mouse).
Q7W642
Q97YW0
Q93YW1
Q65833
Q9UL03
Q9UL03
Q9UL03
Q97YH2
Q87PW8
Q97YH3
Q87743
Q87743
Q87743
Q87743
Q87711
Q87711
Q87711
Q9772C9
Q91711
Q9772C9
Q917711
Q9772C9
Q98Y73
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Q98MJ2
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SEQUENCE FROM N.A.
STRAIN=BALB/c;
MEDLINE=99306687; PubMed=10380019;
MEDLINE=99306687; PubMed=10380019;
                                                                                                                             PRELIMINARY;
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Q925S9
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                                                                                                                                           October 6, 2004, 16:23:13; Search time 36.8596 Seconds (without alignments) 94.160 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                      1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL 25:*

1: Sp archea:*
2: Sp bacteria:*
3: Sp fungi:*
4: Sp human:*
5: Sp invertebrate:*
5: Sp mammal:*
5: Sp mammal:*
5: Sp phage:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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55
1 RASQSIGTNIH 11
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Match Length DB
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OBmwwl scarites su Q8mx00 dicaelus am Q88st3 lactobacill Q98mj2 rhizobium l

127 AA

ô Gaps ., 78.2%; Score 43; DB 11; Length 127; 72.7%; Pred. No. 0.9; .ive 1; Mismatches 2; Indels Ouery Match
Oust Local Similarity 72.72, 19,
Best Local Similarity 72.73, 1 RASQSIGTNIH 11 |||| || |:| 44 RASQDIGINLH à ୍ଷ

Q92559 mus musculu Q8vijó mus musculu Q8vijó mus musculu Q8uoal pyrococcus Q80tu3 mus musculu Q86tv3 coenorhabdi Q7yxu6 caenorhabdi Q5pa8 xanthomonas Q8ukjo agrobacteri Q9azb3 lactobacill Q5gG methanosarc Q33542 clivia mini Q9f6m9 carboxydoth Q8ty39 tribolium c Q7wi08 bordetella

092559 0801J0 0801J0 0801J3 0801J3 0801J3 0955V8 0787U6 0787U6 097B3 097B3 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09558 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 09568 095

108 2112 302 11186 132 299 304 428 428 1440 139

Description

Score

Result

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Pfam; PF00607; Gag p24; 1.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                        6; Conservative
                                                                                                                                                                97 RACQDVGTELH 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RASQSIGTNIH 11
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                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2261;
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                                                                                                 Query Match
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                                                                                                                        Matches
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MEDLINE=96409289; PubMed=8814271;

Wloch N.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
Wloch N.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
Wloch D.K., Inmunol. 26:225-223 (1996).

EMEL, J. Immunol. 26:225-223 (1996).

EMEL, U59155; AAB02917.1; -

PIR, A3933; A33933.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

Fam: PF00047; igy 1.

SMART; SM00406; iGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ishidashi T., Kanehori K., Takiguchi S., Kusano J., Watanabe M., Fulimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Salto K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Fulii A., Oshima A., Sugiyama A., Kawakani B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 11; Length 108;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NEDO human CDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK091495; BAC03676.1; -.
GO; GO:0003676; P:nucleic acid binding; IEA.
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_D24.
InterPro; IPR00916; Retrov capsid_C.
InterPro; IPR001878; ZAF_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                      108 AA; 11859 MW; 68506D75613DBFBE CRC64;
                                                 Q8VIJO;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-DNA light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ34176.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 AA
                                      108 AA
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                                      PRT;
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Query Match
Best Local Similarity 60.v.,
Best Local 6; Conservative
                                      PRELIMINARY;
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                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                              NCBI_TaxID=10090;
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SEQUENCE
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Q8NB65
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
Nakajima D., Nagase T., Ohara O., Koga H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R GO; GO:00162015; AAL81822.1; -..

R GO; GO:0005215; Fitransporter activity; IEA.

R GO; GO:0006810; Pitransport; IEA.

R GO; GO:0006810; Pitransport; IEA.

R Dfan; PF02653; BPD transport

R PF0263; BPD transport

R Dfan; PF02653; BPD transport

R Dfan; PF02654;
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Pred. No. 40;
5; Mismatches 1; Indels
                                                                                                                                                                   67.3%; Score 37; DB 4; Length 212; 54.5%; Pred. No. 27;
                                                                                                                                                                                                                            3; Indels
PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZnF C2HC; 1.
PR0STTE; PS50158; ZF_CCHC; 1.
Hypothetical protein.
SEQUENCE 212 AA; 23378 MW; 2070DE43BD5EE228 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBUDA1;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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01-JUN-2003 (TrEMBLrel, 24, Last seg
01-OCT-2003 (TrEMBLrel, 25, Last ann
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Y43B11AL.2
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Q7YXU6
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"Prediction of the coding sequences of mouse homologues of KIAA gene:
II. The complete nucleotide sequences of 400 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
DNA Res. 10:35-48(2003).
EMBL; AK122345; BAC65627.1; -.
Interpro; IPR003613; Znf_modRING.
Pfam; PR04564; U-box; 1.
SMART; SM00504; Ubox; 1.
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II.L., Tsitrin T., Xim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blutt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.,
"Oryza sativa chromosome 10 BAC OSJNBAO062C05 genomic sequence.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1186;
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66.7%; Pred. No. 1.8e+02;
cive 2; Mismatches 1; Indels
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SEQÜENCE 1186 AA; 134813 MW; 2FC25DC03820A175 CRC64;
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Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitted (MAX-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AC084023, AAN05573.1; -.
EMBL, AC017110, AAP54523.1; -.
Hypochetical protein 1
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Last sequence update)
Last annotation update)
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Best Local Similarity 85.7
Matches 6; Conservative
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SQSLGLNVH 71
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Best Local Similarity
6, Conserva
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RESULT 7

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Watersforn R.,
Direct Submission.";
STRAIN-Bristol N2;
Watersforn R.,
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

ELL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO2479; ARK68485.1;
R MYRPEP; V43B11AL.2; CE28261 to membrane; IEA.

RO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

RO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

RO; GO:0001586; F:C-protein coupled receptor protein signalin. .; I
INTERFORM IPRO00276; GPCR Rhodopsin.

ROSITE; PS50262; GPROTEIN RECEP F1.2; 1.

PROSITE; PS50262; GPROTEIN RECEP F1.2; 1.
                                                                                                                               Y43B11AL.2.
Caenorhabditis elegans.
Eukaryota, Matazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
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                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Cordes M., Maupin R.;
"The sequence of C. elegans cosmid Y43B11AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Y43B11AL.2.
                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Y43B11AL.2.
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80.0%; Pred. No. 63;
iive 0; Mismatches
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  PRT;
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
PRELIMINARY;
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SEQUENCE FROM N.A.
                Q965V8;
01-DEC-2001
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Query Match
Best Local Similarity
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SEQUENCE 428 AA:
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STRAIN-ATCC 33913
MEDLINE-2202145; PubMed=12024217;
MEDLINE-22022145; PubMed=12024217;
MEDLINE-22022145; PubMed=12024217;
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolnin M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Faria J.B., Ferreira R.C.C., Gruber A.,
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                    65.5%; Score 36; DB 5; Length 304; 80.0%; Pred. No. 64;
        Cordes M., Maupin R.; "The sequence of C. elegans cosmid Y43B11AL."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                             [5]
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Waterston R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        Wilson R.; Jull-2003) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. Hypothetical protein. SEQUENCE 304 AA; 34724 MW; 7F7F6C54C4F69589 CRC64;
                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                               Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
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                                                                                                                                   Submitted (JUN-2001)
                                                                                                                                                                                                                                 Waterston R.;
Submitted (NOV-2002)
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Best Local Similarity
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                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2; Waterston R.;
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STRAIN=Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydroxylase,
MBTG OR XCC1598,
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                                                                                                                                                                                                                                                                                    Wilson R.;
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Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Sprinda L.M.F., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Trindade dos Sancos M., Truffi D., Tsai S.M., White F.F.,
Setubal J.C., Kitajima J.P.;
Comparison of the genomes of two Xanthomonas pathogens with differing
Not specificities.";
Nature 417:459-463(2002).
EMBL, ABM10892.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21608550; PubMed=11743193; MeDLINE=21608550; PubMed=11743193; MeDLINE=21608550; PubMed=11743193; MeDLINE=21608550; PubMed=11743193; MeDLINE=21608550; PubMed=1., Wood G.E., Almeida N.F. Jr., Woo L., Cohen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McCelland E., Palmieri A., Raymond C., Rouse G., Sanphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The genome of the natural genetic engineer Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 16; Length 428;
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     428 AA; 47012 MW; FA7C59345838FFE9 CRC64;
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GO; GO:0046821; C:extrachromosomal DNA; IEA.
Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 440 AA; 48826 WW; 583770DD1576D6F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium Tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBUKJO;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atusil2.
ATUSIL2 OR AGR PAT 166.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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75 RARQKIGVSIH 85
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65.3%; Score 36; DB 16; Length 440; 54.5%; Pred. No. 97;

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Amaryllidaceae,
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Gonzalez J.M., Robb F.T.,
Gonzalez J.M., Robb F.T.,
A genomic survey of the extreme thermophilic, CO-utilizing bacterium
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF244664, ARG25533.1;
GO, GO:0016740; Firtransferase activity; IEA.
GO, GO:0016740; Piatransferase activity; IEA.
GO, GO:0006084; Piatransferase activity; IEA.
GO, GO:0016740; Piatransferase
GO, GO:0016740; Firtransferase
GO, GO:0016740; Piatransferase
GO, GO:0016740; Piatransferase
GO, GO:0016740; Piatransferase
FREGUENCE 11 1

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SEQUENCE 211 AA; 23149 MW; C3038601E0C79E82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Damme E.J., Smeets K., Van Leuven F., Peumans W.J.;
"Molecular cloning of mannose-binding lectins from Clivia miniata.";
Plant Mol. Biol. 24:825-830(1994).

EMBL, L16512; AAA19911.1;
PIKS, R43762.

ARA19911.1;
GO, GO:0005529; F:sugar binding; IEA.

InterPro: IRF001460; Blectin.

Frank, PF01453; Agglutini. 1.

SMART; SM00108; B_lectin; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
4-hydroxybutyrace CoA transferase (Fragment).
Carboxydothermus hydrogenoformans.
Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
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Pred. No. 53;
1; Mismatches 2; Indels
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855FD8A3FF7F0B5A CRC64;
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Last annotation update)
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(TrEMBLrel. 01, I
(TrEMBLrel. 25, I
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70.0%;
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Clivia miniata.
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       KGSDSIGRNLH 100
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169
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01-NOV-1996
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01-OCT-2003
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SIGNAL
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Q39542
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STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;

STRAIN=22120827; PubMed=12125824;

MEDLINES-2120827; PubMed=12125824;

Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Brutaggemann H., John and J., Overbeek R., Klenk H.-P., Gunsalus R.P.,

Fritz H.-J., Gottschalk G.,

"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Archhaea; Buryarchaeota; Buryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2209;
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EMBL, AF195900, AAK27908.1; -.
SEQUENCE 1434 AA; 158446 MW; 0EB8B5A863BC4C2C CRC64;
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J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
EMBL, ABO13243, AAM2988.1;
Hypotherical protein; Complete proteome.
SEQUENCE 139 AA; 16170 MW; 28AF39CBEFCD9752 CRC64;
                                                                                                                                                                                                                                                                                                                                               Q9AZB3;
01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Putative minor tail protein.
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GO: GO:00056354; C:nucleus; IEA.

GO: GO:0006355; P:requiation of transcription, DNA-dependent; IEA.

InterPro; IPR001827; Antennapedia.

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Prints; PR00025; ANTENNAPEDIA.

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Galant R., Carroll S.;
"Evolution of a transcriptional repression domain in an insect Hox
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.
Query Match 63.6%; Score 35; DB 2; Length 211; Best Local Similarity 70.0%; Pred. No. 68; Msmatches 7; Conservative 2; Mismatches 1; Indels
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Search completed: October 6, 2004, 16:33:57 Job time: 41.8596 secs

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Mack T.G.A., Reiner M., Beirowski B., Mi W., Emanuelli M., Wagner D.
Thomson D., Gillingwater T., Court F., Conforti L., Fernando F.S.,
Tarlton A., Andressen C., Addicks K., Magni G., Ribchester R.R.,
Perry V.H., Coleman M.P.;
"Wallerian degeneration of injured axons and synapses is delayed by a
UD-64b/Nmac chimeric gene.";
Nat. Neurosci. 4:1199-1206(2001).
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Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/Ola; TISSUE=Brain;
MEDLINE=20481916; PubMed=11027338;
MCDIINE=20481916; PubMed=11027338;
MCDIINE=20481916; PubMed=11007338;
Wagner D., Perry V. H., Coleman M.P.;
"A Ufd2/D4Colete chimeric protein and overexpression of Rbp7 in the slow Wallerian degeneration (WidS) mouse.";
                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko C., Hatakeyama S., Mateumoto M., Yada M., Nakayama K., Nakayama K.I.; "Characterization of the mouse gene for the U-box-type ubiquitin
                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ubiquitin conjugation factor E4 B (Ubiquitin-fusion degradation
protein 2) (Ufd2a).
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MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                                                                                                                                                                                                                                                                 PTM: Proteolytically cleaved by caspases during apoptosis. Cleaved efficiently at Asp-123 by caspase-6 and granzyme B. Cleaved with approximately 10-fold less efficiency at Asp-109 by caspase-3 and caspase-7 (By similarity).

MISCELLANBOUS: In strain C57BL/Ola, an 85-kb region on chromosome 4 containing Numat and Ube4b is triplicated. Ube4b becomes linked to Numat and encodes a fusion protein located in the nucleus which is responsible for the delayed Wallerian degeneration of injured
FUNCTION: Binds to the ubiquitin moieties of preformed conjugates and catalyzes ubiquitin chain assembly in conjunction with E1, E2, and E3 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        axons in CS7BL/Ola.
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R MGD; MGI:1927034; UD64b.

R GO; GO:000151; C:ubiquitin ligase complex; TAS.

R GO; GO:000151; C:ubiquitin ligase complex; TAS.

R GO; GO:0003754; F:chaperone activity; NAS.

R GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.

R GO; GO:000641; P:ubiquitin conjugating enzyme activity; TAS.

R GO; GO:000641; P:ubiquitin conjugating enzyme activity; TAS.

R GO; GO:000641; P:upiquitin and/or maintenance; NAS.

R GO; GO:0042787; P:protein folding; NAS.

R GO; GO:0042787; P:protein folding; NAS.

R GO; GO:0042787; P:protein tubiquitination during ubiquitin-dep. .; T

R GO; GO:0042787; P:protein folding; NAS.

R Fam; PPO4564; U-box; 1.
                                                                                                                                                              AMENDIA: DE SIMILATION SUBMIT SUBMIT SUBMIT IN THE SUBMIT IN THE SUBCELLULAR LOCATION: CYTOPIASMIC.

TISSUE SPECIFICITY: Expressed predominantly in neuronal
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EMBL, AF260926, AAG17287.1; -1260926, AAG17287.1; -1260924, AB083492.1; -1260924, AB08324, BAC5686.1; -1260924, AB083249, BAC5686.1; -1260925, AB083289, BAC5686.1; JOINED.
EMBL, AB083250, BAC5686.1; JOINED.
EMBL, AB083250, BAC5686.1; JOINED.
EMBL, AB083251, BAC5686.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB08326; BAC56586.1; JOINED. BMBL; AB083270; BAC56586.1; JOINED. BMBL; AB083271; BAC56586.1; JOINED. BMBL; AR083271; BAC56586.1; JOINED. BMBL; AK029214; BAC5658.1; JOINED. BMBL; AK02658.1; JOINED. BMBL; AK026588.1; JOINED. BMBL; AK02658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC56586.
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Pfam; PF04564; U-box; 1.
SMART; SM00504; Ubox; 1.
Ubl conjugation pathway.
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can
   (BY CASPASE-3 AND CASPASE-7)
                                                   (BY CASPASE-6 AND GRANZYME B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The human homologue of the yeast polyubiquitination factor Ufd2p cleaved by caspase 6 and granzyme B during apoptosis."; Biochem. J. 361:587-595(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, MUTAGENESIS SPOUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, MUTAGENESIS ASP-121 AND ASP-123, AND CLEAVAGE BY CASPASES.
MEDLINE=2164175; Pubmed=11802788;
MAHORRY J.A., Odin J.A., White S.M., Shaffer D., Koff A., Casciola-Rosen L., Rosen A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             095155; 075169; 095338; 0960D4; Q9BYI7; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last amoutation update) Ubiquitin conjugation factor E4 B (Ubiquitin-fusion dactor E4 B (Ubiquitin-fusion degradation protein 2) (Homozygously deleted in neuroblastoma-1). UBEAB OR UFD2 OR HDNBI OR KIAA0684.
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                                                                                                      L -> P (IN REF. 1).

D -> E (IN REF. 3; BAC26672).

S -> T (IN REF. 3; BAC26672).

C -> Y (IN REF. 1).

E -> K (IN REF. 3; BAC26672).

E -> K (IN REF. 3; BAC26672).
                                                                                                                                                                                                                                                                                                            Length 1173;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1112-1302 FROM N.A.
Barrow I.K.-P., Boguski M.S., Touchman J., Spencer F.,
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                               ; DB 1;
: 18;
                        SIMILARITY).
CLEAVAGE (BY CAS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                            Score 37; DB 1
Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1302 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Substantia nigra;
Kageyama H., Ohira M., Nakagawara A.;
"Human ubiquitination factor E4/UFD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                                                                                                                               67.3%;
                                                                                                                                                                                                                                                                                                                                       66.78;
                                                                                                                                                                                                                                                         133302
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                             697
                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
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                                                                                                            298 29
408 40
674 67
697 69
753 75
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                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
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                                                                                                                                                                                             CONFLICT
                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                            CONFLICT
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UB4B HUMAN
                                                      SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAYAGE (BY CASPASE-3 AND CASPASE-7).
CLEAYAGE (BY CASPASE-6 AND GRANZYME B).
Missing (in isoform 3).
Missing (in isoform 2).
Missing (in isoform 2).
/FIId=VSP 007102.
/FIId=VSP 007102.
/FIId=VSP 007103.
/FIId=VSP 007103.
/FIId=VSP 007103.
/FIId=VSP 007103.
/FIId=VSP 007103.
                                                                                                                                                                                                                       Isode-095155-3; Sequence=VSP_007101, VSP_007102, VSP_007103;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Highest expression in ovary, testis, heart and skeletal muscle. Expression is low in colon, thymus and peripheral blood leukocytes. Almost undetectable in lung and spleen.
PTM: Proteolytically cleaved by caspases during apoptosis. Cleaved efficiently at Asp-123 by caspases during apoptosis. Cleaved efficiently at Asp-123 by caspases and granzyme B. Cleaved with approximately 10-fold less efficiency at Asp-109 by caspase-3 and
FUNCTION: Binds to the ubiquitin moleties of preformed conjugates and catalyzes ubiquitin chain assembly in conjunction with E1, E2, and E3 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D->A: ABOLITION OF CLEAVAGE BY CASPASE-6.
NO EFFECT ON CLEAVAGE BY GRANZYME B.
D->A: ABOLITION OF CLEAVAGE BY CASPASE-6
                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE UBIQUITIN CONJUGATION FACTOR E4 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005737; C:cycoplasm; ISS.
GO; GO:000151; C:ubiquitin ligase complex; TAS.
GO; GO:000151; C:ubiquitin ligase complex; TAS.
GO; GO:0001899; F:chaperone activity; ISS.
GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
GO; GO:0004810; F:ubiquitin conjugating enzyme activity; TAS.
GO; GO:0006915; P:apoptosis; IDA,
GO; GO:0006457; P:protein folding; ISS.
GO; GO:0006457; P:protein biquitination during ubiquitin-dep.
GO; GO:00042787; P:protein ubiquitination during ubiquitin-dep.
GO; GO:000911; P:response to UV; IDA.
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Pred. No. 20;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6BAA80984B03E43B CRC64;
                                                      -1- SUBUNIT: Interacts with Vcp (By similarity).
-1- SUBCELULIAR LOCATION: Cytoplasmic (By similarity).
-1- ALTERNATIVE PRODUCTS:
--- Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ubl conjugation pathway, Alternative splicing. DOMAIN 1231 1293
                                                                                                                                                                                         IsoId=095155-2; Sequence=VSP_007102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND CASPASE-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND GRANZYME
                                                                                                                                                  IsoId=095155-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF331520; AAK69622.1; -.
EMBL; ABC43117; AAADC233.1; -.
EMBL; ADC28839; BAB40446.1; -.
EMBL; AL096841; CAC42394.1; -.
EMBL; AD014584; BAA31659.2; -.
EMBL; AF091093; AAC72962.1; ALT_SEQ.
Genew; HGNC:12500; UBE49.
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Best Local Similarity 66.7%;
Matches 6; Conservative 2
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SMART; SM00504; Ubox; 1
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                                                                                                                                  Name=1;
                                                                                                                                                                                                             Name=3;
                                                                                                                                                                         Name=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEATALL=970.

WEATALLE TO CHUTCHET C.M..

COllins M., Connor R., Cronin A., Davis P., Hiddell T., Fraser A.,

Gentles S., Goble A., Handin N., Harris D., Hiddeld T., Hodgson G.,

A. Gones L., Jones M., Leather S., McDonald S., McLean J.,

A. Jones L., Jones M., Leather S., McDonald S., McLean J.,

A. Mooney P., Moule S., Mungall K., Munrphy L., Niblett D., Odell C.,

A. A. Diver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

A. A. Diver K., O'Neil S., Mangall K., Munrphy L., Niblett D., Odell C.,

A. A. Diver K., O'Neil S., Mangall K., Munrphy L., Niblett D., Odell C.,

A. A. Diver K., O'Neil S., Mangall K., Maren T., Whitehead S.,

A. Diver K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

A. Taylor K., Taylor R.G., Arrt R., Robben J., Grymonprez B.,

A. Moodward J., Volckaert G., Arrt R., Robben J., Grymonprez B.,

Meltjens I., Vanstreels B., Rieger M., Schaefer M., Moteller A.,

B. Goffeau A., Cadieu E., Dreans S., Gloux S., Lelaure V., Mottler S.,

Goffeau A., Cadieu E., Dreans S., Gloux S., Lelaure V., Mottler S.,

A. Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Moreno S., Armstrong J., Forsburg S.L.,

Certutti L., Lowe T., Moccomble W.R., Paulsen I., Potashkin J.,

Mathe 415:811-880(2002).

Mathe 415:811-880(2002).

L. SIMILARITY: TO YEAST YDLII7W.
                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales; Schizosaccharomycetacese;
Schizosaccharomyces.
                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein C9G1.06c in chromosome I.
                                                                                                                                                                         886 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, Z98763; CAB11490.1; -.
PIR; T39229; T39229.
HSSP; P29355; ISEM.
GGeneDB_SPombe; SPAC9G1.06c; -.
INTERFO; IPR001422; SH3.
InterPro; IPR002331; Trnsglumase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PSS0002; SH3; 1.

Hypothetical protein; SH3 domain.

6 67 SH3.
                                                                                                                                                                                                                  5-JUL-1998 (Rel. 36, Created)
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                                                                                                                                                                         STANDARD;
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SMART; SM00460; TGC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00018; SH3; 1.
     3 SOSIGINIH 11
                                              50 SOSLGLNVH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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014302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Swiss Webster; TISSUE=Connective tissue;
MEDINIP=93200524; PubMed=8453108;
MEDINIP=93200524; PubMed=8453108;
Heusel J.W., Scarpati E.M., Jenkins N.A., Gilbert D.J., Copeland N.G.,
Shapiro S.D., Ley T.J.;
Molecular cloning, chromosomal location, and tissue-specific
expression of the murine cathepsin G gene.";
Blood 81:1614-1623 (1993).
                                                                                                                                                                        Gaps
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Nakamura N., Tsuru A., Hirayoshi K., Nagata K.;

Nakamura N., Tsuru A., Hirayoshi K.,

Nakamura N., Tsuru A., Hirayoshi K.,

Nakamura N., Tsuru A., Hirayoshi K.,

Nayata K.;

Nayatoloi deukemia cells. Regulation during differentiation and identity with cathepsin G.";

Bur. J. Blochen. 205:1947-994 (1922).

-I. FUNCTION: This vienentin-specific protease may regulate the reorganization of vienetin filaments; occurring during cell differentiation, movement and mitosis.

-I. CATALYTIC ACTIVITY: Specificity similar to chymotrypsin C.

-I. SUBCELLULAR LOCATION: STRONGIY ASSOCIATED WITH MEMBRANES.

-I. SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBR-2003 (Rel. 41, Last amocation update)
Cathepsin G precursor (EC 3.4.21.20) (Vimentin-specific protease)
                                                                                                                                                                        .,
                                                                                               Match 65.5%; Score 36; DB 1; Length 886; Local Similarity 85.7%; Pred. No. 21; es 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kulmburg P., Baumruker T., Werner F.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Leaden X A.H.
Huang R., Aveskogh M., Hellman L.T.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
610 POLY-SER.
98262 MW; DOC4879C1882E869 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AA
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EMBL; X70057; CAA49661.1; -.
EMBL; X78544; CAA55290.1; -.
PIR; S40162; 840162.
HSSP; P09311; 1CGH.
MEROPS; S01.133; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                             451 SVGTNIH 457
607 6
886 AA;
                                                                                                                                                                                                                                           5 SIGTNIH 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATG MOUSE
P28293;
                                                                                                   Query Match
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CATG_MOUSE
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                                                                                                                                                                        Matches
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DNA recombination; Coiled coil; Complete proteome.

DOMAIN 29 88 COILED COIL (FOTENTIAL).
SEOUENCE 432 AA; 48721 MW; 73DF45A996A2F692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 13:6499-6513(1985).
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z00021; CAA77316.1; -. PIR; A01899; K3HU41.
                                                                                                                            Local Similarity 66.7 les 6; Conservative
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21
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128
128 AA;
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ID KV3K HUMAN
AC P06311;
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Schence 293:2009-2008(2001).
-!- FUNCTION: Involved in DNA recombination (By similarity).
-!- SIMILARITY: Belongs to the rmuc family.
                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
MEDLINE=21442074; Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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Rickettsiaceae, Rickettsieae, Rickettsia.
                           InterPro; IPR099033; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR00125; Crypsin, 1.
Pfunts; PR00722; CrymorryPsin, 1.
PRNTS; PR00722; CrymorryPsin, 1.
PROSITE; PS00026; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DIS; 1.
PROSITE; PS00135; TRYPSIN PIS; 1.
Hydrolase; Schine procease; Zymogen; Glycoprotein; Signal; Intermediate filament; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 1; Length 261; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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-> G (IN REF. 4)
-> P (IN REF. 4)
-> P (IN REF. 4)
5EFAIAGE1051D7FC CRC64;
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BY SIMILARITY.
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ACTIVATION PEPTIDE.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MAX recombination protein rmuC homolog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%;
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Best Local Similarity 70...
7, Conservative
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149 RVSQSRGTNV 158
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          MGD; MGI:88563; Ctsg.
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Q92GR5;
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RMUC RICCN
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                                                               Gaps
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PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .<del>.</del>
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
63.6%; Score 35; DB 1; Length 432; 66.7%; Pred. No. 16; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; Length 128; Pred. No. 7.7; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14070 MW; CC8957F0FE3B9012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-07M-1988 (Rel. 06, Created)
01-07M-1988 (Rel. 06, Last sequence update)
15-0UL-1999 (Rel. 38, Last amnotation update)
1G Aspa chain V-III region IARC/BL41 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
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GO, GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; F:antigen binding; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
Imminglobulin V region; Signal.
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RX STRANSBERGALEY;
RX Adams LOD. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA damstides P.G., Scherer S.E., Holt R.A., Galle R.F.,
Adamstides P.G., Scherer S.E., Holt R.A., Galle R.F.,
Button G.G., Wortman J.R., Yandall M.D., Zhango Q., Chan L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basud A., Baxendale J., Bayaktaroglu L., Beaaley E.M.,
Ballew R.M., Banos P.V., Berman B.D., Bhandari D., Boshakov S.,
Berkova D. Botcham M.R., Buck J. Brokstein P., Berman B.D., Bhandari D., Beabley E.M.,
R. Bencon K.Y., Bencos P.V., Berman B.D., Bhandari D., Boshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R. Cabler A., Domy E.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Durbin K.J. Gabrelian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Alochon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Plaicohman W.,
R. Gong F., Gorrell J.H., Gu Z., Gtan P., Harris M.L., Harvey D.A., Heiman T.J., Herrandez J.R., Houston K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J. Lin X.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J., Martis M.L., Harves B., McIntoex T.C., McLeod M.P., McPherson D.L.,
Menut S.M., Moy M., Murphy B.L., Muzhy D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Mohaer K.C., Muzhy D.M., Nelson D.L.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,
Rolls E., Spradling A.C., Schoeler F., Wang X.,
Williams S.M., Woodage T., Worley K.C., Wu Shenger B.,
Williams S.M., Woodage T., Worley K.C., Wu Shenger B.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,
Rolls R.M., Whyer S.W., Wolld M., Velly K.C., Will Schole M., Shing B.,
Rolls R.C., Siden-Kiamos I., Shupski M., Shupski M.P.,
Rolls R.C., Siden-Kiamos I., Shupski M., Velly R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS.
MEDLINE-22426069; PubMed=12537572;
Missa S., Campbell K.S.,
Missa S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Fradecky P., Huany Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mutations are the Trf cluster cause a premeiotic defect in the brosophila male germ line.";
Submitted (FBB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
11-OCT-2003 (Rel. 42, Last sanctation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last sequence update)
12-OCT-2003 (Rel. 42, Last sequence update)
13-OCT-2003 (Rel. 42, Last se
                                                                                                 252 AA.
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
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RESULT 8
TRFP_DROME
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                                                                                                                                                                                                                                   STRAIN=Berkeley; TISSUE=Embryo; Stableton M., Carlson J.W., Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J.W., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Paragas V., Park S., Patel S., Phouanenavong S., Man K.H., Yu C., Lewis S.E., Rubin G.M., Celniker S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: May regulate transcription of class II genes through association with the RNA polymerase II-SRB complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 40.8 kDa protein in RHKI-PETI12 intergenic region.
YBL081W OR YBL0722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Component of an RNA polymerase II-SRB complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obermaier B., Gassenhuber J., Piravandi E., Domdey H., "Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevisiae chromosome II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 252;
Pred. No. 15;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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EMBL; BT003473; AA039476.1; --
FlyBase; FBqn0013531; Trfp.
Transcription regulation; Nuclear protein.
CONFLICT 220 220 H -> Q (IN REF. 1).
SEQUENCE 252 AA; 27862 NW; 608AB5A43DAC52F5 CRC64;
                                                                                                                          Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity). --
-:- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 AA
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MEDLINE=96076635; PubMed=7502586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                        systematic review.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
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P38180;
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InterPro; IPR003607; Met_phsphohydro.
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                                                                                                                                                                                                                                           Query Match
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Matches
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       SO KW 
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Nat. Biotechnol. 20:118-1123(2002).
1- SIMILARITY: Belongs to the dGTPase family. Subfamily 2.
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=22297686; PubMed=12368813;
MedCalberg J.F., Paulsen I.T., Naleon K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Deboy R.T., Dodson R.J., Duwyam L.A., Watte D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Wanthevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Muller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Bacteria; Protechacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Deoxyguanosinetriphosphate triphosphohydrolase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.8%; Score 34; DB 1; Length 368; 77.8%; Pred. No. 23; 17.8%; Pred. 1; Mismatches 1; Indels
one almost entirely hydrophobic and the other extremely asparagine-serine rich.", Yeast 10:1251-1256(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40767 MW; D52EAA7AD85C5D14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 AA
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InterPro; IPR006261; dGTP_triPase.
InterPro; IPR006674; HD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE015690; AAN55516.1; -.
TIGR; SO2485; -.
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X79489, CAA56026.1; -. EMBL, Z35842, CAA84902.1; -. EMBL, M89908; AAA75353.1; -. PIR, S46601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GermOnline; 138516; -. SGD; S0000177; YBL081W. Hypothetical protein. SEQUENCE 368 AA; 4076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 SSSIGTNIN 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBEEA2;
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DGT1 SHEON
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SEQUENCE OF 10-536 FROM N.A.

STATISTORY Columbia, TISSUB-Callus;

MEDLINE-94211851; PubMed=7512729;

MEDLINE-94211851; PubMed=7512729;

MEDLINE-94211851; PubMed=7512729;

The Arabidopsis thaliana apurinic endonuclease Arp reduces human transcription factors Fos and Jun.";

Transcription factors Fos and Jun.";

Proc. Natl. Acad. Sci. U.S.A. 91:3299-3303(1994).

Tedox factor: Is multifunctional and may be involved both in DNA repair and in the regulation of transcription.

Tedox factor: Is multifunctional and may be involved both in DNA repair and in the regulation of transcription.

Tedox factor: Is multifunctional and may be involved both in DNA repair and in the regulation of transcription.

Tedox factor: Is multifunctional and may be involved both in DNA repair and in the regulation of transcription.

Tedox factor: Is multifunctional unsaturated sugar and a product with a printing a 3'-terminal unsaturated sugar and a product with a creminal 5'-phosphate.

Terminal 5'-phosphate.

Terminal 5'-phosphate.

Terminal 5'-phosphate or seen in the leaves.

Thissue specificity: Expressed in the siliques, flowers, and stems.

A high level expression is seen in the leaves.

This IMPARITY: Contains 1 SAP domain.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Apurinic endouclease-redox protein (DNA-(apurinic or apyrimidinic site) lyase) (EC 4.2.99.18).
ARP OR REF OR AT2G41460 OR T26J13.5.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J. B., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                        61.8%; Score 34; DB 1; Length 441; 54.5%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                  Indels
PEam; PF01966; HD; 1.
SWART: SW00471; HDc; 1.
TIGRPAMS; TIGN01353; dGTP triPase; 1.
Hypothetical protein; Hydrolase; Complete proteome.
SEQUENCE 441 AA; 50619 NW; CIDA17F434ED9514 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 AA.
                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                   Local Similarity 54.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 RASEQLGLNSH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-88274327; PubMed=2839594;
MEDLINE-88274327; PubMed M.A., Davison A.J., Dolan A., Frame M.C.,
MCGOCh D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.B., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(198).
-!- FUNCTION: Tegument protein.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                     EMBL, AC04211; AAF36067.2; --
BEMBL, AC04221; AAF36067.2; --
WormPep; Y76B12C.7; CE2993.

GO; GO:0005847; C:mRNA cleavage and polyadenylation specificity factor.
GO; GO:0005378; P:mRNA polyadenylation; NAS.
Interpro; IPR04871; CPSF_A_C.
Pfam; PF03178; CPSF_A_L.
Pfam; PF03178; CPSF_A, 1.

mRNA processing; Nuclear protein; RNA-binding.
SEQUENCE 1454 AA; 162716 MW; DEFEF8BB2FFBD16F CRC64;
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                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; Length 1454; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 3164; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 3164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X14112, CAA32311.1; -.
PIR, I30085, WMBEH6.
InterPro; IPR006928; Herpes teg N.
InterPro; IPR005210; Herpes_U336.
Pfam; PP04843; Herpes_U336; 1.
Pfam; PF03586; Herpes_U336; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8%;
                                                                                                                                                                                                                                                                                                                                                                     63.68;
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Best Local Similarity 66...
G. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1307 RAAINIGTNIN 1317
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEGU HSV11
P10220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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                         DDA BARRAR AND DDA BARRAR AND BAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA repair; Lyase; Nuclear protein.
DOMAIN 1 278 HIGHLY CHARGED; INCREASES THE AFFINITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=5239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGNESIUM OR MANGANESE (BY SIMILARITY)
GENERAL BASE (BY SIMILARITY).
5C1FC17EA991D27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cleavage and polyadenylation specificity factor, 160 kDa subunit (CPSF 166 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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Pred. No. 33;
1; Mismatches 2; Indels
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STRANT=Bristol N2;
Cordes M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP ENDONUCLEASE.
                                                                                                                                                                                                                                 Pfam; PF03372; Exo endo phos; 1.
Pfam; PF02037; SAP; 1.
TMRAT; SM0513; SAP; 1.
TIGREAMS; TIGR00195; exoDNase_III; 1.
TIGREAMS; TIGR00633; xth; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_2; 1.
PROSITE; PS00728; AP_NUCLEASE_F1_2; 1.
PROSITE; PS00728; AP_NUCLEASE_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARP FOR DNA
                         or send an email to license@isb-sib.ch)
                                                           EMBL; AC004625; AAC23731.1; -.
EMBL; X76912; CAA54234.1; -.
PIR; T02441; T02441.
HSSP; P27695; 1E9N.
InterPro; IPR001097; APendonclsel.
InterPro; IPR001089; Exo endo phos.
InterPro; IPR00488; ExoIII_xth.
InterPro; IPR00334; SAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60260 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313
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279
313
327
527
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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ACT_SITE
SEQUENCE
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Q9N4C2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                         Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; Weissenbach J., Ehrlich S.D., Sorokin A.; The complete genome sequence of the lactic acid bacterium Lactococcus Tatis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
-: SIMILARITY: Belongs to the UPF0237 family.
                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Goldfien R., Carson D.A., "Cloning and sequence determination of a human rheumatoid factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UDL-1999 (Rel. 38, Last annotation update)
IG kappa chain V-III region CLL precursor (Rheumatoid factor).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A77ED01657C149DE CRC64; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  light-chain genē.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1;
Pred, No. 8.4;
                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0237 protein yjhc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B86743; B86743.

HAWAP; MF_01054; -; 1.

InterPro; PR002911; ACT.

Hypothetical protein; Complete proteome. SEQUENCE 87 AA; 9282 MW; A77ED01657C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
 PRT;
                                                                                                                                                                                                           STRAIN=1L1403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86177570; PubMed=3083417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006329; AAK05044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                       CUHC OR LL0946.
LACLA
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P04207;
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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0
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FRANEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRANEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 129;
Pred. No. 13;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14275 MW; SC13B411BE60CC14 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00047; ig; 1. ZaNARY; SMO4066; IGy. 1. PROSITE, PSE0835; IG LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%;
                                                                                                                                                                                                                                                                                                        EMBL; M12740; AAA58992.1; -.
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les 6; Conservative
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6, 2004, 16:30:27 Search completed: October Job time: 8.75439 secs

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Gaps

1 RASOSIGTNI 10

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44 RASOSVSNNL

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 16:23:59 ; Search time 11:5789 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-8 55 1 RASQSIGTNIH 11 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Iq light chain V r	Ig kappa chain pre	kappa chain	Ig kappa chain V r	kappa chain pr	Ig kappa chain V r	Ig kappa chain V r	anti-glycoprotein	anti-glycoprotein	kappa chain	F	ы	g kappa chain V	Б	Ig kappa chain - h	ס	ם	0	g kappa chain	d hypot			>	g kappa	binding 1	hypothetical prote	G	tical p	protein
. QI	PH1082	KVMSL7	44	ö	6	4	ユ	B45722	2	7	C45722	PH0867	837511	JE0243	~	31	20	σ,	57	17	22	82	$\sim$	2655	4376	235	016	783	57
DB	2	H	7	7	7	7	7	0	~	7	7	~	~	N	7	N	~	~	7	0	7	0	7	0	7	7	N	N	17
Query Match Length	87	ч	128	O	Н	O	$\circ$	0	0	Э	0	95	91	н	122	2	4,	$\leftarrow$	N	4	æ	96	88	н	163	S	9	m	œ
Query		6.06	。		ö	76.4	ė.	76.4	è.	ů,	4.	ά.	。	ö	69.1	σ.	ь О	7.	۲.	'n.	'n.	۳,	ω,	ω.	۳.	ω,		ო	m.
Score	50	20	50	48	44	42	42	42	42	42	41	40	39	39	38	38	38	37	37	36	36	35	32	35	35	35	35	32	35
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kappa chain V		kappa chain V		kappa chain V	kappa chain V	kappa chain V	kappa chain V	Ig kappa chain V r	kappa chain V						
S78489	S34099	S16834	S16836	S16839	S16828	S16835	C28195	S16824	S16829	S34098	537525	837527	PH0868	PL0267	A28195
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83	84	86	86	86	98	98	98	98	86	87	9	93	95	106	107
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ij	61	61	61	61	61	61	61	61	61	61	61	61	61	61.	61
_			4	4	34	34	34	34	34	34	34	34	34	34	34
	34	34	m	m											

### ALIGNMENTS

RESULT 1	
Filabs [d light chain V region (clone 165.54) - mouse (fragment)	
C, Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 21-Jan-2000	
C, Accession: PH1082	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B (	ve B
A; Reference number: PH0971; MUID: 92381444; PMID: 1512540	
A; Accession: PH1082	
A;Status: nucleic acid sequence not shown	
A; Molecule type: mRNA	
A; Residues: 1-87 <til></til>	
A; Experimental source: B cell, strain [NZB x NZW] Fl	
C; Superfamily: immunoglobulin V region; immunoglobulin homology	
C; Keywords: immunoglobulin	
F;6-80/Domain: immunoglobulin homology <imm></imm>	
Query Match 90.9%; Score 50; DB 2; Length 87;	
Similarity 90.9%; Pred. No. 0.0045;	
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
OV 1 RASOSIGTNIH 11	

## 1 RASQSIGTNIH 11 |||||||||||||| 14 RASQSIGTSIH 24 Š DP

INVESTATION OF CONDITION OF CON

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Gaps

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Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26346
R;Stark, S.E.; Caton, A.J.
A;Stark, S.E.; Caton, A.J.
A;Title: Antibodies that are specific for a single amino acid interchange in a protein eparace number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Accession: B43413

R; Tomiyama, Y; Brojer, B.; Ruggeri, Z.M.; Shattil, S.U.; Smiltneck, J.; Gorski, J.; Kume J. Biol. Chem. 267, 18085-18092, 1992

J. Biol. Chem. 267, 18085-18092, 1992

A; Title. A molecular model of RGD ligands. Antibody D gene segments that direct specificity A; Reference number: A43413; WUID:92388177; PMID:1517241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
C;Accession: S00996
                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-114 <STR>
A,Cross-references: EMBL:M27750; NID:g185914; PIDN:AAA58912.1; PID:g553479
A,Note: this sequence was determined from the germline gene
C,Genetics:
                                   Ristraubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G. Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A;Title: Two unusual human immunoglobulin V-kappa genes.
A;Reference number: S00996; MUID:89134397; PMID:2852016
A;Accession: S00996
                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;1.19/Domain: signal sequence #status predicted <SIG>F;120-114/Product: Ig Rappa chain V region #status predicted <WAT>F;20-114/Product: Ig stapa chain V region #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; Pl C. Superfanily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;14-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-104 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: sequence extracted from NCBI backbone (NCBIP:112818)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 76.4%; Score 42; DB 2; Length 102; Local Similarity 72.7%; Pred. No. 0.24; es 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 2;
Pred. No. 0.11;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 RASOSIGSSLH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RASOSIGTNIH 11
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A, Molecule type: mRNA
A, Residues: 1-102 <STA>
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Matches
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R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0445
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                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain precursor V-I region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                    Gaps
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A.Cross-references: GB:L02347
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
C.Keywords: heterotetramer; immunoglobulin
C.Keywords: heterotetramer; immunoglobulin
F:11000main: signal sequence #status predicted <81G>
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F:26-100/Domain: immunoglobulin homology <1MM>
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A;Coss.references: GB:M21907; NID:g197071; FIDN:AAA38907.1; FID:g197072<br/>
C;Superfamily: immunoglobulin V region; immunoglobulin homology<br/>
C;Keywords: heterotetramer; immunoglobulin<br/>
F;16-90/Domain: immunoglobulin homology <IMM>
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0
                                                                                             Score 50; DB 1; Length 115;
Pred. No. 0.0061;
1; Mismatches 0; Indels
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81.8%; Pred. No. 0.015;
iive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 2; Length 128
Pred. No. 0.0069;
1; Mismatches 0; Indels
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C;Species: Homo sapiens (man)
              F;36-110/Domain: immunoglobulin homology <IMM>F;43-108/Disulfide bonds: #status predicted
                                                                                             90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.98;
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                       Conservative
                                                                                                                                                                                                            1 RASQSIGTNIH 11
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Matches 9; Conserv
                                                                                                                          Best Local Similarity
Matches 10; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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                                                                                                Query Match
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Gaps

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PID:91334075

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C,Accession: PH0867
R,Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
R,Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
A,Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A,Reference number: PH0862; MUID:92078875; PMID:1660528
A,Accession: PH0867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-95 - MANA
A; Residues: 1-95 - MANA
C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Sayberds: heterotetramer; immunoglobulin
F; 1-23/Region: framework 1
F; 1-23/Region: framework 1
F; 1-6-90/Domain: immunoglobulin homology < IMM>
R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K. Gene 51, 13-19, 1987
A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine A;Reference number: A91572; MUID:87248058; PMID:3110009
A;Rocession: A26471
A;Molecule type: MRNA
A;Residues: 1-138 ABUC>
A;Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;1-20/Domain: signal sequence #status predicted <NGP>
F;21-138/Product: Ig kappa chain V region #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 22.Sep.1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 C,Accession: C45722 C,Accession: C45722 C,Accession: C45722 C,Accession: C45722 C,Accession: C45722 C,Accession: C7,A; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasq. J. Virol. 67, 489-496, 1993 E,Accession: C48722; MUD:93100833; PMID:7677958 C,Accession: C45722 C,Accession: C45722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - mouse (f
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C.Species: Mus musculus (house mouse)
C.Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1892 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence extracted from NCBI backbone (NCBIP:120591) C;Superfanily: immunoglobulin V region; immunoglobulin homology C;Keywords: glycoprotein F;Ie-90/Pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
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                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2;
Pred. No. 0.34;
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63.6%; Pred. No. 0.41;
cive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3
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                                                                                                                                                                                                                                                                                                                                                                     76.48;
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Best Local Similarity 72...
Best Local 8; Conservative
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Best Local Similarity 63.6
Matches 7, Conservative
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                                                                                                                                                                                                                                                                                                                                                         anti-glycoprotein. H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr c) Species: Mus musculus (house mouse)
C)Species: Mus musculus (house mouse)
C)Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C)Accession: B45722
B/Simpson, J-A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu J. Vizol. 67, 489:496, 1993
A/Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: B45722
A;Accession: B45722
A;Accession: B45722
A;Accession: Compared with conceptual translation
A;Residues: 1-107 <SIN>
A;Note: sequence extracted from NCBI backbone (NCBIP:120590)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;16-90/Domain: immunoglobulin homology <IMM>
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Ig kappa chain precursor V region (MAK33) - mouse
C;Species: Mus musculus (house mouse)
C;Date: O5-Jun-1988 #sequence_revision O5-Jun-1988 #text_change 23-Jul-1999
C;Accession: A26471
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                                                                  Length 104;
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0.25;
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Pred. No. 0.25;
1; Mismatches
                                                                  Score 42; DB 2
Pred. No. 0.25;
1; Mismatches
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76.4%; Score 42; DB
Best Local Similarity 72.7%; Pred. No. 0.25
Matches 8; Conservative 1; Mismatches
           F;13-87/Domain: immunoglobulin homology <IMM>
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ilarity 72.7%;
Conservative
                                                                  Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity
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Search completed: October
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R;Klein, U.; Kueppers, R.; Rajewsky, K.
Rubmitted to the EMBL Data Library, September 1993
A;Description: Human IgM(*)IgD(*) cells, the major B cell subset in the peripheral blood A;Reference number: S37501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain NIG93 precursor - human
Cispecies: Homo sapiens (man)
Cidate: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
CiAccession: UE0243
RiAlim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Tabubitted to JIPID, November 1998
A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A; Reference number: UE0243
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                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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840370
19 kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-91 «KLB»
A; Cross-references: EMBL.226600; NID:g405664; PIDN:CAA81354.1; PID:g405665
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                      Gaps
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R;Xlein, R.; Jaenichen, R.; Zachau, H.G.

A;Itle: Emmunol. 23, 3248-3271, 1993

A;Itle: Empressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: $40312; MUID:94080891; PMID:8258341
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A;Residues: 1-215 cALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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     Score 40; DB 2; Length 95; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2; Length 91;
Pred. No. 0.89;
2; Mismatches 1; Indels
                                                      1; Indels
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                                                                                                                                                                                                                                                                           Ig kappa chain V region (V-kappa 3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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Pred. No. 2.3;
                                                   2; Mismatches
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Best Local Similarity 70.0%;
Matches 7; Conservative 5
Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 70.0
70.0
                                                                                                     1 RASQSIGTNIH 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
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JE0243
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 16:24:54; Search time 19.4912 Seconds (without alignments)
29.135 Million cell updates/sec

Title: US-09-635-974A-8
Sequence: 1 RASQSIGTNIH 11
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued_Patents_AA:*

abase : Issued Patents_AA:*
1: /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	-	equence 53,	Sequence 53, Appl	equence 4,	equence 4,	equence 4,	Sequence 4, Appli	4,	ģ	ω̈	equence 10	9	equence 8,	equence 10	equence 6,	æ	equence 10	æ	equence 8,	œ	'n	4	m	8	equence 1,	1, Appl	_
QI	US-08-476-176B-53	-08-127-721A-5	-08-485-	US-08-800-198-4	-09-296-5	-08-476-1	US-08-127-721A-4	-08-485-	-08-47	-476-176B-	38-476-176B-	US-08-127-721A-6	US-08-127-721A-8	18-127-721A-	38-485-246A-	-08-485-	-08-485-24	.19	-09-296-59	US-08-653-402B-8	1	-07-942-245-4	US-08-525-539A-3	-463-2	-08-107-669D-	-08-472-788	US-08-477-531B-1
oth DB			11 3																								107 2
% Query Match Length	100.0	100.0	100.0	0	ö	。	100.0		100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0				٠	87.3	7.	87.3	87.3
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니쇼	Seguence 4, Appli Seguence 9, Appli	Sequence 40, Appl Sequence 4, Appli	Sequence 1, Appli	7	11	7	Sequence 99, Appl	7	Sequence 20, Appl	Sequence 112, App	Sequence 2, Appli	19,	Sequence 21, Appl
US-08-082-842A-1 US-07-942-245-4	99	US-08-232-081B-40 US-07-956-399-4	US-09-244-369B-1	38-276-852-	US-08-899-575-113	US-08-899-575-113	US-09-472-087-99	PCT-US95-08743-113	0	US-09-472-087-112	US-09-096-244-2	US-08-436-463-19	US-08-436-463-21
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107	11	107	244	96	96	96	96	96	155	155	4	100	103
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87.	85.	85.		10	0	80	0	0	0	0	78		76
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7 7 7 8 8	30	33	3.4	9 9	3.7	38	39	40	41	42	43	44	45

### ALIGNMENTS

nal antibodies against an sctype Department ersion #1.25  /P2/CIP 5; DB 2; Length 11; o. 0.0001; tches 0; Indels 0;	•	Gaps
antibodies YPe jon #1.25  ion #1.25  /CIP  /CIP  /CIP  ion #1.25  ion #1.25  ion #1.25	re e	,,
RESULT 1  US-08-476-176B-53  Sequence 53, Application US/08476176B  Patent No. 5958708  GENERAL INFORMATION: PAPLICANT: Kolbinger, Frank APPLICANT: Saldanha, Jose TITLE OF INVENTION: immunoglobulin interpretation of the control of	1476-176B-53  476-176B-53  th No. 5958708  ERAL INFORMATION: PELICANT: Kolbinger, Frank PELICANT: Kolbinger, Frank PELICANT: Saldanha, Jose PELICANTON: immunoglobulin isotype ORRESPONDENCE S.  STREET: 59 Route 10 CITY: Back Hanover STREET: 59 Route 10 CITY: Back Hanover COMPUTER: New Jersey COUNTRY: USA ZIP: O7936-1080  MENDI APPLICATION DATA: PELICANTON NUMBER: US/08/476,176B FILING DATE: 25-SEPTEMBER-1992 FILING DATE: 1080-MATION: FELEFRAX: (908) 277-4306 CHENERY OR SEQ ID NO: 53: ERGUENCE CHARACTERISTICS: ERGUENCE CHARACTERISTICS: ERGUENCE CHARACTERISTICS: ERGUENCE CHARACTERISTICS: ERGUENCE CHARACTERISTICS: ERGUENCE TYPE: maino acids TOPPOLOSY: linear	Match Local Similarity 100.0%; Score 55; DB 2; Length 11; Local Similarity 100.0%; Pred. No. 0.0001; es 11; Conservative 0; Mismatches 0; Indels

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Thu Oct 14 09:37:01 2004

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59 Route 10

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ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,
                                                                                                                  ADDRESSEE:
STREET: 22
                                                              ô
                                                                 Gaps
                                                                                                                                                                                                                               RESULT 3
US-08-485-246A-53
US-08-485-246A-53
Sequence 53, Application US/08485246A
Sequence 53, Application US/08485246A
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
ITTLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CONTRESPONDENCE ADDRESSE:
ADDRESSEE: No. 6072035artis Patent Department
        100.0%; Score 55; DB 3; Length 11; 100.0%; Pred. No. 0.0001; ative 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                           RASOSIGTNIH 11
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100.0%; Score 55; DB 3; Length 11; 100.0%; Pred. No. 0.0001;
                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
SOOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY AGENT INFORMATION:
NAME: No. 6072035A, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
MATHER TOWN NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (908) 277-5110
               STATE: New Jersey
COUNTRY: USA
ZIP: 07936-108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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East Hanover
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Gaps o O

0; Indels

Mismatches

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Sequence 4, Application US/08800198
Patent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHWIDT, MATHIAS
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 STATE: VA

COUNTRY: US

ZIP: 22201

COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                     SSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. 12200 CLARENDON BLVD. SUITE 1400
ARLINGTON
JS-08-800-198-4
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RESULT 7
US-08-127-721A-4
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pactor No. 5958708

GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Hardman, No. 5958708man
APPLICANT: Rolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Remanaglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: Bast Hanover
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 55; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09296595A

Sequence 4, Application US/09296595A

Patent No. 6129915

GENERAL INFORMATION:

APPLICANT: WELS, WINFRIED S.

APPLICANT: SCHMIDT, NATHIAS

APPLICANT: SCHMIDT, NATHIAS

TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES

TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES

CURRENT APPLICATION WUMBER: US/09/296,595A

CURRENT FILING DATE: 1999-04-23

CURRENT FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 4

LENGTH: 106

LENGTH: 106

LENGTH: 106

LENGTH: 1079-04-23

CORGANISM: Murine SP.

US-09-296-595-4
REFERENCE/DOCKET NUMBER: SC
TELECOMMINICATION INFORMATION
TELEPHONE: 703-243-6333
TELEFAX: 703-243-641
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                          peptide
NO
                                                                                                                                                                                                                                                                           internal
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                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: pepti
HYPOTHETICAL: NO
FRAGMENT TYPE: inter
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US-08-476-176B-4
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amino acid
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Best Local Similarity 100.
Matches 11; Conservative
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    24 RASQSIGTNIH 34
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                                                                                    US-08-476-176B-6
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US-08-476-176B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08485246A
Patent No. 6072035
GENERAL INPORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Imminoglobulin isotype
CORRESPONDENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4-19276/A/P2/CIP
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 408/127,721
APPLICATION NUMBER: 408/127,721
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035A, Henry P.
REGISTRATION NUMBER: 33,200
REPERENCE/DOCKET NUMBER: 4-19276/A/P
TELECHONICATION INFORMATION:
TELECHONE: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
: JUBERONE: (308) 277-5110
TELBEAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amir:
  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                        TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-127-721A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                           1 RASOSIGTNIH 11
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STREET: 59 Koucc
CITY: Bast Hanover
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-485-246A-4
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1 RASQSIGTNIH 11

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Gaps
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APPLICANT: Hardman, No. 5958708man
APPLICANT: Hardman, No. 5958708man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
ITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708axtis Patent Department
STREET: 59 Route 10
                                                                                            APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
APPLICANT: Raldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 2; Length 127; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 CITY: Bast Hanover STATE: New Jersey CONTRY: USS JONES COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM FOCOMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27.SEPTEMBER: 1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25.SEPTEMBER:1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 59537084, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/F
TELECHONE: (908) 277-5110
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION FOR SEQ ID NO: 6:
Sequence 6, Application US/08476176B Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08476176B Patent No. 5958708
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Gaps
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| Patent No. 6066718
| GENERAL INFORMATION:
| APPLICANT: Hardman, No. 6066718man
| APPLICANT: Kolbinger, Frank
| APPLICANT: Saldanha, Jose
| TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
| NUMBER OF SEQUENCES: 55
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 2; Length 127; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NOWBER:
US/06/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION 1424
PRIOR APPLICATION: 42-SEPTEMBER-1993
TLING DATE: 27-SEPTEMBER-1992
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
RESTSATION NUMBER: 33.200
RESTSATION NUMBER: 33.200
RESTSATION NUMBER: 33.200
RESTSATION NUMBER: 34-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 598708AX; Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECHONENICATION INFORMATION:
TELEPAX: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
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                                                                                                                                                                                                                                            LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-476-1768-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein
US-08-127-721A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RASQSIGTNIH 11
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Sequence 10, Application US/08476176B
Sequence 10, Application US/08476176B
Sequence 10, S958708
Sequence 10, S958708
Sequence 10, S958708
Septicant: Saladanha, Jose
APPLICANT: Saladanha, Jose
TITLE OF INVENTION: immunoglobulin isotype
CORRESPONDENCE: 55
SADRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STREET: New Jersey
COUNTRY: USA
COUNTRY: USA
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: BAP PC COMPATA:
SPELICATION NUMBER: US/08/476,176B
STATE: PAPLICATION DATE:
SPELICATION NUMBER: US/08/476,176B
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                                           COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR PAPLICATION: 435

PRIOR PAPLICATION: DATA:
APPLICATION NUMBER: 08/127,721

FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/552,802

FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGRAY INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1933
APPLICATION NUMBER: US 07/952,802
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  East Hanover
New Jersey
Y: USA
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STREET:
CITY: Ea
STATE: N
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                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08127721A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Raldman, Osee
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08127721A
Sequence 10, Sof6718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Kolbinger, Frank
APPLICANT: Saldana, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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CITY: East Hanover STATE: New Jersey
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COUNTRY: USA

ZIP: 07936-1080

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127,721A

FILING DATE: 27-SEPTEMBER-1993

FILING DATE: 25-SEPTEMBER-1992

ATORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,200

REGISTRATION NUMBER: 33,200

REFERENCE/DOCKET NUMBER: 33,200

REF
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
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US-08-127-721A-10
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US-08-127-721A-8
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| ATTORNEY/AGENT INFORMATION:
| NAME: No. 6072035ak, Henry P. |
| REGISTRATION NUMBER: 4.19276/A/P2/CIP |
| REPRENCE/DCOKET NUMBER: 4.19276/A/P2/CIP |
| TELEPHONE: (908) 277-4310 |
| TELEPHONE: (908) 277-4310 |
| TELEPHONE: (908) 277-4310 |
| TELEPHONE: (908) 277-4306 |
| INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: |
| LENGTH: 127 amino acid |
| TYPE: amino acid |
| TYPE: amino acid |
| TOPOLOGY: linear |
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Wellskin us-09-635-974a-8.rag

October 6, 2004, 16:20:48 ; Search time 55.5789 Seconds (without alignments) 55.921 Million cell updates/sec 1586107 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-635-974A-8 55 1 RASQSIGTNIH 11 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* .: geneseqp1980s:* : geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	0	4	Aab37955 Anti-EGFR	7		90 Light	49 Kappa	8 Kappa	9 Light	4	2 Light	Aar50187 Light cha	1 Light	945 Kappa	Aaw08941 Kappa lig	46 Kappa	3 Карра	1 Light	980	N	33	43	SCFV	35 scFv (225	40 scFv2
SUMMARIES	ΩI	AAY26990	AAY59314	AAB37955	AAU77787	AAW71241	AAR50190	AAW08949	AAW08948	AAY26979	AAY70604	AAR50192	AAR50187	AAR50191	AAW08945	AAW08941	AAW08946	AAW08943	AAY26981	AAY26980	AAY26982	AAW05133	AAW71243	AAY70605	AAW05135	AAW05140
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### ALIGNMENTS

RESULT 1

The invention relates to a method of determining IgE levels in a body fluid sample, by contacting the sample with a reshaped human monoclonal antibody (RA) having a binding affinity about equal to that of the murine CDR-donor antibody TES-C21 produced by the cell line 11133. The antibodies are useful in the diagnosis, prophylaxis and treatment of allergy. This sequence represents the complementarity determining region (CDR) 1 from the light chain variable domain of a reshaped human antibody Diagnosis; IgE; immunoglobulin; body fluid; human; monoclonal antibody; binding affinity; mouse; CDR; complementarity determining region; CDR1 domain reshaped human antibody light chain variable region. new method for determining IgE levels in a sample. Hardman N; AAY26990 standard; protein; 11 AA. Claim 5; Col 67; 19pp; English. (NOVS ) NOVARTIS CORP. (TANO-) TANOX BIOSYSTEMS INC. 92US-00952802. 93US-00127721. 95US-00476176, Saldanha J, Kolbinger F, 24-DEC-1999 (first entry) WPI; 1999-570765/48. Homo sapiens. 07-JUN-1995; 25-SEP-1992; 27-SEP-1993; US5958708-A. 28-SEP-1999 Synthetic AAY26990; allergy. AAY26990 

Query Match

100.0%; Score 55; DB 2; Length 11;

Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.

99US-00312284. 99US-00374028.

14-MAY-1999; 13-AUG-1999; [IMCL-) IMCLONE SYSTEMS INC

Waksal HW;

01-MAY-2000; 2000WO-US011756.

WO200069459-A1

Mus sp.

23-NOV-2000

Anti-EGFR monoclonal antibody L chain V region CDR1 peptide sequence.

12-MAR-2001 (first entry)

AAB37955;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the hypervariable region CDR1 (complementarity determining region 1) of the light chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, color, kidney, bladder, head and neck, overy, prostate or brain. The administration of a suitable antibody to the patient makes the tumour more susceptible to radiotherapy
                                                                                                                                                                                                                                                                                   Hypervariable region, complementarity determining region, CDR, tumour; single chain antibody, growth inhibitor; human, tumourigenesis; therapy, protein receptor tyrosine kinase, light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.
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                   0; Indels
   Pred. No. 0.00023;
Mismatches 0;
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                                                                                                                                                                                                                                                       Light chain hypervariable region, CDR1.
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                                                                                                                                                             AAY59314 standard; peptide; 11 AA
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98US-0085613P.
98US-00206138.
    100.08;
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Best Local Similarity 100.
Matches 11; Conservative
                   Conservative
                                                   RASOSIGINIH 11
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Best Local Similarity
Matches 11; Conserv
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15-MAY-1998;
07-DEC-1998;
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This invention relates to a method for inhibiting the growth of refractory tumours that are stimulated by a ligand of epidernal growth factorized receptor (EGFR) in human patients. The method involves treating the patient with a combination of EGFR/Human EGF-1 (HER1) antegonist, optionally with a chemotherapeutic agent or radiation. The antagonist can be for example a chimeric anti-EGFR monoclonal antibody, C225. The COT CARPHIER1 antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, Eplem, kidney, bladder, head and there, ovary, prostate, brain, pancreas, skin, bone, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence region complementarity determining region 1 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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100.0%; Pred. No. 0.00023;
tive 0; Mismatches 0;
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Gaps ..

AAB37955 standard; protein; 11 AA.

RESULT 3
AAB37955
ID AAB3

1 RASOSIGINIH 11 RASOSIGINIH 11

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New single chain polypeptide that binds to epidermal growth factor receptor - is derived from antibody 14E, used for treatment and diagnosis of cancer or other cell proliferative diseases.
                                                                                                                                                                                                                                                                                                                                      The present sequence represents the light chain variable domain of murine monoclonal antibody 1451. This antibody is active against the human epidermal growth factor receptor (EGF-R). The sequence is used to construct a single-chain polypeptide (scFv) that has binding affinity for an EGF-R. The scFv comprises two segments which contain the binding parts of the heavy and light chain variable domains of the monoclonal antibody 1481. The scFvs of the invention are used to cardinomas (gliomas, melanomas and tumours) that overexpress EGF-R, specifically EGF-RVIII, relative to normal cells, particularly by blocking proliferation of such vitro purging. When the scFv is appropriately labelled, it can be used diagnostically to image cells that express EGF-R, specifically breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody; heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 2; Length 106; 100.0%; Pred. No. 0.0031; ive 0; Mismatches 0; Indels
                                                                                                           Schneider DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain variable region of TES-C21 antibody.
                                                                                                           Vakalopoulou E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/label= CDR 2.
89. 97
/label= CDR 3.
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                        97US-00800198
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Best Local Similarity 100.
Matches 11, Conservative
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18-OCT-1994 (first en
                                                                                                         Schmidt M,
                                                                                                                                                   WPI; 1998-467176/40.
                                                                   (SCHD ) SCHERING AG.
                                                                                                                                                                         N-PSDB; AAV54788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 106 AA;
                        13-FEB-1997;
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Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for treating a mammal with the hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (BGF) family of receptors. The method involves commissering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the antagonist and phototherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal growth factor receptor (BGFR) antagonist by inhibiting EGFR /HERL phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic keratoses, seborrheic keratoses, wartes, keloid scars and eczema stimulated by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 255 antibody light chain (LH) the invention
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                                                                                                                                                                                                                                                                                                                                                                                                     Treating a manmal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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human epidermal growth factor receptor; EGF-R; treatment; carcinoma;
EGF-RvIII; in vitro purging; breast carcinoma; ss.
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hypervariable region; CDR1; EGFR inhibitor.
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                                                                                                                                                                                                             09-AUG-2000; 2000US-00635974.
                                                                                                                                                                   09-AUG-2001; 2001WO-US041647.
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N-PSDB; ABK11443.
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                                                                                    WO200211677-A2
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                                                                                                                          14-FEB-2002
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                                                         07-JUN-1995;
15-DEC-1995;
                                       07-JUN-1996;
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WO9640210-A1
                   19-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kappa; light chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                   Reshaped human monoclonal antibodies can be used in the prophylaxis and/or treatment of allergic reactions in humans. The monoclonal antibodies can also be used for the qualitative or quantitative determination of IgE and for the determination of surface IgE positive B cells. They can provide a long lasting therapeutic effect without inducing immunogenicity as foreign proteins. The CDR's from the variable heavy and light chains of the murine antibody TES-C21 were used in the construction of a molecular model of the variable heavy and light chains for the murine antibody and light chains and light chain framework regions. (Updated numan variable heavy field.) (Updated on 25-MAR-2003 to correct PM field.)
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                                                                                                          New reshaped human monoclonal antibody specific for IgE - used for prophylaxis or treatment of allergic reactions or qualitative or quantitative determn. of IgE.
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                                                           Hardman N, Kolbinger F, Saldanha J;
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/label= CDR_2
57. 88
/label= framework_3
89. 97
/label= CDR_3
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/label= framework_2
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/label= framework_4
                                                                                                                                                  Disclosure; Page 28; 68pp; English.
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'label= framework 1
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                            (TANO-) TANOX BIOSYSTEMS INC. (NOVS ) NOVARTIS AG.
 92US-00952802
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                   (CIBA ) CIBA GEIGY AG
                                                                               WPI; 1994-103410/13.
                                                                                       N-PSDB; AA044714
                                                                                                                                                                                                                                                                                              Sequence 107 AA;
 25-SEP-1992;
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Matches
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Kappa, light chain, reshaped, monoclonal, antibody, 225RA, human, edjdermal growth factor; EGF, receptor; inhibition; growth, tumour; cell, late stage, prostatic; prostate, variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                        Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RA. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
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                                                                                                                                                                                                                              Saldanha JW;
                                                                                                                                                                                                                              Soldstein NI, Giorgio NA, Jones ST,
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/label= framework_3
89. .97
/label= CDR_3
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/label= framework_2
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label= framework 1
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                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
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label= CDR_1
96WO-US009847.
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The invention relates to a method of determining IgE levels in a body fluid sample, by contacting the sample with a reshaped human monoclonal antibody (RA) having a binding affinity about equal to that of the murine CDR-donor antibody TES-C21 produced by the cell line 1113. The antibodies are useful in the diagnosis, prophylaxis and treatment of allergy. This sequence represents the light chain variable domain from the TES-C21 antibody. The fragments encoding the complementarity determining regions are used to generate the reshaped antibodies of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present protein sequence is the Vkappa (kappa chain variable region) of the humanised antibody Hu-901. This is an exemplary anti-IgE (anti-immunoglobulin E) monoclonal antibody produced by hybridoma TES-C21. The heavy and light chains are obtained through RT-PCR using the RNA from the transfectoma cell line producing the chimeric antibody. Humanised anti-IgE genes are incorporated in the genome of a recombinant adenovirus vector as an independent transcriptional unit, and packaged into infectious virus particles. Upon infection of host, the recombinant adenovirus vector will direct the production of either intact anti-IgE antibody or an scFv fragment in the serum, which will bind free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibody-901, Hu-901; Vkappa; kappa chain variable region; anti-19g; anti-1pg; anti-1-munoglobulin E; monoclonal antibody; hybridoma TES-C21; recombinant adenovirus vector; anti-19E antibody; gene therapy; scFv; single chain variable fragment; allergy; antiallergic.
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for determining IgE levels in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vkappa region of humanised antibody Hu-901.
                                        Disclosure; Col 35-36; 19pp; English
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N-PSDB; AAZ52078.
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                       Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (Wab) H325. 225R%, The Mab is specific for the human epidermal growth factor (EGF) receptor. The Mab, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or isplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                            anti-EGF receptor antibody 225 of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 2; Length 107; 100.0%; Pred. No. 0.0032; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain variable domain from antibody TES-C21.
                                                                                                                                                                                                                                          Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hardman N;
                                                                                                                                                                                                                                                                                                                                                  for inhibiting tumour growth, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY26979 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                            and humanised versions of
                                                                                                                                                                                                                                                                                                                                                                                          Claim 29; Fig 21; 112pp; English.
                                                                                                                                                                                  IMCLONE SYSTEMS INC.
MRC COLLABORATIVE CENT
                                                                             96WO-US009847.
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                                                                                                                      95US-00482982.
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93US-00127721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha J, Kolbinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS CORP
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N-PSDB; AAZ28545.
                                                                                                                                                                                                                                                                                       WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 107 AA;
                                                                                                                                                                                                                                               Goldstein NI,
                                                                                 07-JUN-1996;
                                                                                                                      07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
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27-SEP-1993;
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                                        19-DEC-1996
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(MRCC-)
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circulating 1gE, resulting in the reduction of free serum 1gE. The binding of the antibody or fragment to 1gE-bearing B cells may lower 1gE levels by down-regulating 1gE production by these B cells. These methods are useful in the gene therapy of allergic diseases
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New reshaped human monoclonal antibody specific for IgE - used for prophylaxis or treatment of allergic reactions or qualitative or quantitative determn. of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
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                                                                                                                                                                                                          100.0%; Score 55; DB 3; Length 107; 100.0%; Pred. No. 0.0032; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain variable region C21-L3 of reshaped antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/label= CDR 2.
109. .117
/label= CDR 3.
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/label= CDR 1.
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(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
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(first entry)
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                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                   1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                     24 RASQSIGTNIH 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-103410/13.
                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                    Sequence 107 AA;
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Binding-site
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25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP589840-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1994,
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AAR5
DT 25-W
DT 25-W
DT 18-C
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Anti
KW Anti
COX
KX C
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position 3 of the mature protein instead of leucine (positions 21 and respectively of this sequence). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                      Antibody; heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New reshaped human monoclonal antibody specific for IgE - used for prophylaxis or treatment of allergic reactions or qualitative or
                                                                                                          .
                                                                                Length 127;
                                                                   100.0%; Score 55; DB 2; Length 12' 100.0%; Pred. No. 0.0039; Undels
                                                                                                                                                                                                                                                                                                                            Light chain variable region C21-L1 of reshaped antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hardman N, Kolbinger F, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
44. .54
/label= CDR 1.
                                                                                                                                                                                                                                  AAR50187 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 29-30; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70. .76
/label= CDR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109. .117
/label= CDR 3.
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92US-00952802.
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(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quantitative determn. of IgE.
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                            Local Similarity 100.
                                                                                                                                     1 RASOSIGTNIH 11
                                                                                                                                                              54
                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                              44 RASQSIGTNIH
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                                                     Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1993;
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25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                      25-MAR-2003
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                                                                                Query Match
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Matches
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Sequence 127 AA;

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Pred. No. 0.0039; Mismatches 0; Indels

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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reshaped human monoclonal antibodies can be used in the prophylaxis and/or treatment of allergic reactions in humans. The monoclonal antibodies can also be used for the qualitative or quantitative determination of IgE and for the determination of surface IgE positive B cells. They can provide a long lasting therapeutic effect without inducing immunogenicity as foreign proteins. This sequence is a slightly modified version of C21-L1 described in AAR50187, having aspartic acid at position 60 of the mature protein (position 80 of this sequence) instead of serine. (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003 to correct PM field.)
                               Gaps
                                                                                                                                                                                                             Antibody, heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New reshaped human monoclonal antibody specific for IgB - used for prophylaxis or treatment of allergic reactions or qualitative or quantitative determn. of IgE.
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        100.0%; Score 55; DB 2; Length 127;
100.0%; Pred, No. 0.0039;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                             Light chain variable region C21-L2 of reshaped antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha J;
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                       AAR50191 standard; protein; 127 AA.
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                                                                                                                                                                                                                                                                                    44. .54
/label= CDR 1.
70. .76
/label= CDR 2.
109. .117
/label= CDR 3.
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(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
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92US-00952802
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                                                                                                                                                               (revised)
(first entry)
   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kolbinger F,
                                                 1 RASOSIGINIH 11
                                                                     RASOSIGINIH
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N-PSDB; AAQ44715.
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                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                             25-MAR-2003
18-OCT-1994
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                                                                                                                                           AAR50191;
                                                                                                   RESULT 13
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Length 127;

DB 2;

Score 55;

100.08;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kappa; light chain; murine; mouse; monoclonal; antibody; C225; human; pepidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric; L7'CL; leader sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the kappa light chain variable region of the chimeric monoclonal antibody (MAb) C225, with the modified leader sequence from the kappa light chain of L7.CL MAb. C225; is specific for the human epidermal growth factor (EGF) receptor. C225, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage spotstatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                 Kappa light chain variable region of C225 antibody.
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ID AAW08945 standard; protein; 127 AA.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                        1 RASOSIGINIH 11
                                                                                                       44 RASQSIGTNIH 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT49344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus, spp.
Homo sapiens.
Synthetic.
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15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric.
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                                                                                                                                                                                                                                                                                                         AAW08945;
                                                                                                                                                                                               RESULT 14
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AAW08941
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Kappa; light chain; murine; mouse; monoclonal; antibody; M225; human;
epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell;
late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the kappa light chain variable region of the murine monoclonal antibody (MAb) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                      Kappa light chain variable region of M225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                     Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                     Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example IV; Fig 13; 112pp; English.
                                                                                                                                                                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                               95US-00482982.
                                                                                                                                                                                                                                                                  96WO-US009847.
                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-051897/05.
N-PSDB; AAT49338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 127 AA;
                                                                                                                                                                                                       WO9640210-A1.
                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                             07-JUN-1995;
15-DEC-1995;
                                          27-AUG-2003
18-SEP-1997
                                                                                                                                                                                                                                    19-DEC-1996,
               AAW08941;
                                                                                                                                                                            Mus sp.
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.. 0

0; Gaps

100.0%; Score 55; DB 2; Length 127; 100.0%; Pred. No. 0.0039; ative 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 11; Conservative

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Search completed: October 6, 2004, 16:29:46 Job time : 56.5789 secs

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6, 2004, 16:34:15; Search time 37.3684 Seconds (without alignments) 51.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/prodate/2/pubpaa/USO7_PUBCOMB.pep:*
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18: /cgn2_6/prodate/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1351062 segs, 321799191 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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25
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                          October
                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## STIMMARTES

Description	Sequence 34, Appl	Sequence 10, Appl	30,	Sequence 40, Appl	Sequence 101, App	Sequence 101, App	Sequence 30831, A	Sequence 191046,	Sequence 3, Appli	Sequence 18, Appl	Sequence 229773,	Sequence 25, Appl	Sequence 28, Appl	Sequence 38, Appl	Seguence 129, App
ΠD	US-09-798-689-34	US-09-996-954B-10	US-10-239-656-30	US-10-239-656-40	US-10-374-600-101	US-10-374-531-101	US-10-029-386-30831	US-10-424-599-191046	US-10-379-151-3	US-10-379-151-18	US-10-424-599-229773	US-09-991-470-25	US-10-239-656-28	US-10-239-656-38	US-10-453-698-129
	10	10	12	12	12	15	14	12	16	16	12	0	12	12	13
Length	1. 49	9	7	7	7	7	19	46	61	61	88	107	107	107	107
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25
Result No.		7	٣	4	2	9	7	<b>6</b> 0	σ	10	11	12	13	14	15
	Query Score Match Length DB ID	Score Match Length DB ID  Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 34,	Score Match Length DB ID Description 25 100.0 6 10 US-09-996-954B-10 Sequence 14,	Query       Score       Match Length DB ID       Description         25 100.0       6 10 US-09-798-689-34       Sequence         25 100.0       6 10 US-09-96-954B-10       Sequence         25 100.0       7 12 US-10-239-656-30       Sequence	Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 34, 25 100.0 6 10 US-09-996-954B-10 Sequence 10, 25 100.0 7 12 US-10-239-656-40 Sequence 40, 25 100.0 7 12 US-10-239-656-40 Sequence 40, 25 100.0 7 12 US-10-239-656-40 Sequence 40, 25 100.0 7 12 US-10-239-656-40	Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 34, 25 100.0 6 10 US-09-996-954B-10 Sequence 10, 25 100.0 7 12 US-10-239-656-30 Sequence 40, 25 100.0 7 12 US-10-374-600-101 Sequence 101, 25 100.0 7 12 US-10-374-600-101 Sequence 101, 25 100.0 7 12 US-10-374-600-101	Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 34, 25 100.0 6 10 US-09-996-954B-10 Sequence 10, 25 100.0 7 12 US-10-239-656-30 Sequence 30, 25 100.0 7 12 US-10-339-656-40 Sequence 40, 25 100.0 7 15 US-10-374-600-101 Sequence 101, 25 100.0 7 15 US-10-374-501-101 Sequence 101, 25 100.0 7 15 US-10-374-501-101 Sequence 101, 25 US-10-374-501-101	Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 34, 25 100.0 6 10 US-09-996-954B-10 Sequence 10, 25 100.0 7 12 US-10-239-656-30 Sequence 30, 25 100.0 7 12 US-10-239-656-40 Sequence 40, 25 100.0 7 12 US-10-374-600-101 Sequence 101, 25 100.0 7 15 US-10-374-531-101 Sequence 101, 25 100.0 19 14 US-10-029-386-30831 Sequence 101, 25 100.0 19 14 US-10-029-386-30831 Sequence 3083	Query         Query         Booker Match Length DB ID         Description           25         100.0         6         10         US-09-798-689-34         Sequence 34, Sequence 10, Sequence 30, Sequence 30, Sequence 10, Sequence 40, Sequence 40, Sequence 40, Sequence 40, Sequence 40, Sequence 101, Sequence 3083           25         100.0         7         12         US-10-374-600-101         Sequence 101, Sequence 101, Sequence 3083           25         100.0         7         15         US-10-374-531-101         Sequence 3083           25         100.0         6         10         10         10         10           25         100.0         7         12         US-10-374-531-101         Sequence 3083           25         100.0         7         12         US-10-374-599-13104         Sequence 3083	Score Match Length DB ID Description  25 100.0 6 10 US-09-798-689-34 Sequence 25 100.0 6 10 US-09-798-58-10 Sequence 25 100.0 7 12 US-110-239-656-40 Sequence 25 100.0 7 12 US-110-239-656-40 Sequence 25 100.0 7 12 US-110-334-650-101 Sequence 25 100.0 7 15 US-110-374-531-101 Sequence 25 100.0 19 14 US-110-029-386-30831 Sequence 25 100.0 6 1 US-110-029-386-30831 Sequence 25 100.0 6 16 US-110-379-151-3 Sequence 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  25         100.0         7         12         US-10-339-656-30         Sequence           25         100.0         7         12         US-10-374-600-101         Sequence           25         100.0         7         15         US-10-374-600-101         Sequence           25         100.0         19         14         US-10-374-600-101         Sequence           25         100.0         19         14         US-10-374-599-191046         Sequence           25         100.0         46         12         US-10-379-151-3         Sequence           25         100.0         61         16         US-10-379-151-3         Sequence           25         100.0         8         12         US-10-379-151-3         Sequence	Score Match Length DB ID Description  25 100.0 6 10 US-09-798-689-34 Sequence 25 100.0 6 10 US-09-798-689-34 Sequence 25 100.0 7 12 US-10-239-656-30 Sequence 25 100.0 7 12 US-10-239-656-40 Sequence 25 100.0 7 12 US-10-374-600-101 Sequence 25 100.0 7 15 US-10-374-531-101 Sequence 25 100.0 7 15 US-10-374-531-101 Sequence 25 100.0 19 14 US-10-029-386-30831 Sequence 25 100.0 61 16 US-10-379-151-3 Sequence 25 100.0 61 16 US-10-379-151-3 Sequence 25 100.0 107 9 US-10-379-151-3 Sequence 25 100.0 107 9 US-09-991-470-25 Sequence 25 100.0 107 9 US-09-991-470-25 Sequence	Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 25 100.0 6 10 US-09-96-954B-10 Sequence 25 100.0 7 12 US-10-239-656-40 Sequence 25 100.0 7 12 US-10-239-656-40 Sequence 25 100.0 7 12 US-10-239-656-40 Sequence 25 100.0 7 15 US-10-374-501-101 Sequence 25 100.0 19 14 US-10-23-386-30831 Sequence 25 100.0 19 14 US-10-23-386-30831 Sequence 25 100.0 61 16 US-10-379-151-18 Sequence 25 100.0 61 16 US-10-379-151-18 Sequence 25 100.0 107 12 US-10-379-556-28 Sequence	Score Match Length DB ID  25 100.0 6 10 US-09-798-689-34 Sequence 25 100.0 7 12 US-10-239-656-30 Sequence 25 100.0 7 12 US-10-239-656-30 Sequence 25 100.0 7 12 US-10-339-656-30 Sequence 25 100.0 7 12 US-10-339-656-30 Sequence 25 100.0 7 12 US-10-34-600-101 Sequence 25 100.0 7 15 US-10-34-600-101 Sequence 25 100.0 19 14 US-10-079-386-30831 Sequence 25 100.0 61 16 US-10-424-599-191046 Sequence 25 100.0 61 16 US-10-379-151-18 Sequence 25 100.0 88 12 US-10-379-151-18 Sequence 25 100.0 107 12 US-10-39-656-28 Sequence 25 100.0 107 12 US-10-39-656-28 Sequence 25 100.0 107 12 US-10-39-656-38 Sequence 25 100.0 107 12 US-10-39-656-38 Sequence 25 100.0 107 12 US-10-39-656-38 Sequence

Sequence 113, App Sequence 10, App Sequence 120, App Sequence 113, App Sequence 113, App Sequence 113, App Sequence 22, App Sequence 23, App Sequence 23, App Sequence 21, App Sequence 11, App Sequence 11, App Sequence 5, App Sequence 11, App Sequence 11, App Sequence 5, App Sequence 11, App Sequence 11, App Sequence 12, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 5, App Sequence 11, App Sequence 57, App Sequence 5606, Ap Sequence 15496, Ap Sequence 1549, Ap
US-10-374-600-113 US-10-374-600-114 US-10-374-600-114 US-10-379-189-4 US-10-379-189-4 US-10-379-189-4 US-10-379-189-4 US-10-374-511-113 US-10-374-600-20 US-10-374-600-20 US-10-374-600-20 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-600-10 US-10-374-610-10 US-10-374-610-10 US-10-374-610-10 US-10-374-610-10 US-10-374-610-10 US-10-374-610-10 US-10-374-610-10 US-10-10-66-88-606 US-09-764-864-154-10
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## ALIGNMENTS

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WESUNIT INCRANTION: US/09798689

| Sequence 34, Application US/09798689
| Sequence 34, Application US/09798689
| Publication No. US2003103973A1
| GENERAL INFORMATION: Use the control of the control of
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1 ASESIS 6

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
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2 ASESIS 7
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US-10-374-600-101
                                                                             US-10-239-656-40
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Publication No. US20040038339A1

GENERAL INFORMATION:

APPLICANT: RITHMULLER, GERT

APPLICANT: BITHMULLER, GERT

APPLICANT: BORSCHERT, KARIN

APPLICANT: BORSCHERT, KOMANIN

APPLICANT: HOFMEISTER, KOMANIN

APPLICANT: HOFMEISTER, ROMANIN

APPLICANT: HOFMEISTER, ROMANIN

APPLICANT: HOFMEISTER, ROMANIN

APPLICANT: HOFMEISTER, ROMANIN

APPLICANT: MAYER MOUNTON WINTING SITE

TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX

FILE REFERENCE: 029976/0106

FILE REFERENCE: 2003-03-06

CURRENT FILLING DATE: 2003-03-06

PRIOR APPLICATION NUMBER: PCT/FP01/03414

PRIOR APPLICATION NUMBER: EP 00106467.4

PRIOR FILING DATE: 2001-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D OTHER INFORMATION: hybridoma 8G7C10 variable light chain CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 10;
100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT , ORGANISM: Homo sapiens-Rodent Chimera US-09-996-9548-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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                                             US-09-996-954B-10
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US-10-239-656-30
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APPLICANT: KIETHWULLER, FALF
APPLICANT: KIETHWULLER, GERT
APPLICANT: BORGCHERT, KATRIN
APPLICANT: BORGCHERT, KATRIN
APPLICANT: BORGCHERT, KATRIN
APPLICANT: BORGCHERT, KATRIN
APPLICANT: HOFWEISTER, ROBERT
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
TITLE OF INVENTION: WINDER: W10/239,656
TITLE REFERENCE: 029376/0106
CURRENT FILING DATE: 2003-06
PRIOR APPLICATION NUMBER: PCT/EP01/03414
PRIOR APPLICATION NUMBER: EP 00106467.4
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTIN VARIABLE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SSOFTWARE: PATENTIN VARIABLE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D; OTHER INFORMATION: hybridoma 6E5A7 variable light chain CDR2
US-10-239-656-40
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Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
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STATE: New York
COUNTRY: US
ZIP: 100404
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 MD storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0;
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RAPPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                           Sequence 40, Application US/10239656
Publication No. US20040038339A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & 1
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
1 ASESIS 6
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8 ASESIS 13
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Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
ATILE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTELE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 12; Length 7; 100.0%; Pred. No. 1.2e+06; Live 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 425-7200
TELEFAX: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECTLE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/09/973,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
PILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon & STREET: One Broadway
CITY: New York STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Best Local Similarity
Matches 6; Conserv
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| ASESIS 7
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US-10-029-386-30831

US-10-029-386-30831

Sequence 30831, Application US/10029386

Publication No. US20030194704A1

GRADEAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

CURRENT APPLICATION UNMBER: US/10/029,386

CURRENT FILING DATE: 200112-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

LENGTH: 19
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                                                                                                                                                                                                                                                                                                          Length 7;
                                                                                                                                                                                                                                                                                                                                                   Indels
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                    TYPE: amino acid
STRANDEDESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                   LENGTH: 7 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
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Squence 229773, Application US/10424599
Squence 229773, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Voring baid K
APPLICANT: Cao Voringwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: 1000 Number: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
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Fatent No. US20020173477A1

GENERAL INFORMATION:

APPLICANT: Ruey S. Liou

ITILE OF INVENTION: ANTI-IGE GENE THERAPY

FILE REFERENCE: 99-5

CURRENT FILING DATE: 2001-11-20

FRIOR APPLICATION NUMBER: BALLIER APPLICATION NUMBER: 09/397,569

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-16

NUMBER: OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25-

LENGTH: 107
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                                                                                                                                                                          Query Match 100.0%; Score 25; DB 16; Length 61; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 88;
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US-10-424-599-229773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 12;
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
                                                                           FEATURE:
, OTHER INFORMATION: Cloned Antibody CDR Sequences
US-10-379-151-18
                          TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 6, Conservative
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ORGANISM: human/murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-229773
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LENGTH: 88
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        LENGTH: 61
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Sequence 3, Application US/10379151

Publication No. US20040175692A1

GENERAL INFORMATION:
APPLICANT: Hackion Pharmaceuticals, Inc.
APPLICANT: Boodish, Katherine S.
APPLICANT: McMhirter, John
IITLE OF INVENTION: CHRONIC LYMPHOCYTIC LEUKEMIA CELL LINE
FILE REFERRNCE: 60 CIP (1087-43 CIP)
CURRENT APPLICATION NUMBER: US/10/379,151

CURRENT FILING DATE: 2001-12-10

PRIOR FILING DATE: 2001-12-10

PRIOR FILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.2

LENGTH: 61

TWIND: DATE
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Fublication No. US20040175692A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
TILE OF INVENTION CHRONIC LYMPHOCYTIC LEUKEMIA CELL LINE
TILE OF INVENTION CHRONIC LYMPHOCYTIC LEUKEMIA CELL LINE
CURRENT APPLICATION NUMBER: PCT/US01/47931
PRIOR APPLICATION NUMBER: PCT/US01/47931
PRIOR APPLICATION NUMBER: US 60/254,113
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Score 25; DB 16; Length 61; Similarity 100.0%; Pred. No. 1e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Length 46;
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                       ; CTHER INFORMATION: Clone ID: PAT_MRT3847_14533C.1.pep
US-10-424-599-191046
                                                                                                                                                                                                                                                           Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
// OTHER INFORMATION: Cloned Antibody CDR Sequences US-10-379-151-3
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191046
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: artificial sequence
                                                                                                         TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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2 ASESIS 7
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US-10-379-151-18
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                                                                                                                                                                                                                                                                              APPLICANT: RIETHMULLER, GERT
APPLICANT: RIETHMULLER, RAILF
APPLICANT: WATRIN
APPLICANT: WARRY, WANTRIN
APPLICANT: WASCHEL, ROMAN
APPLICANT: WARRY, WONKA
APPLICANT: WARRY, WONKA
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
CURRENT APPLICATION NUMBER: US/10/239,656
CURRENT APPLICATION NUMBER: EP 00106467.4
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 28
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/10239656
Publication No. US20040038339A1
GENERAL INFORMATION:
APPLICANT: RIFTHMULLER, GERT
APPLICANT: RIFTHMULLER, GERT
APPLICANT: MYPER, PRIFT
APPLICANT: MYPER, PALK
APPLICANT: MYPER, MAIN
APPLICANT: MYPER, MYRA
APPLICANT: MYPER; MYRA
APPLICANT: MYPERS: US/10/239,656
CURRENT APPLICATION NUMBER: US/10/239,656
CURRENT APPLICATION NUMBER: DO3-06
PRIOR APPLICATION NUMBER: PO10-03-26
PRIOR APPLICANTON NUMBER: ED 00106467.4
SEQ ID NO 38
SEQ ID NO 38
LEBGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D; OTHER INFORMATION: hybridoma 8G7C10 variable light chain US-10-239-656-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                   Sequence 28, Application US/10239656
Publication No. US20040038339A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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51 ASESIS 56
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D; OTHER INFORMATION: hybridoma 6E5A7 variable light chain US-10-239-656-38
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                                                                                                                                 Gaps
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                                                                                    Length 107;
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                                                                               Query Match 100.0%; Score 25, DB 12, Length 1 Best Local Similarity 100.0%; Pred. No. 1,9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                   Sequence 129, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SEQ ID NO 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: October 6, 2004, 17:09:05 Job time: 37.3684 secs
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Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                            51 ASESIS 56
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                                                                                                                                                                        1 ASESIS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                            RESULT 15
US-10-453-698-129
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Query Match
Best Local Similarity
Matches 6; Conserv
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US-08-232-081B-5
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254, Appl

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Sequence 4
Sequence 8
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-195-868-23
US-09-195-868-23
US-09-195-868-23
US-08-232-081B-40
US-08-232-081B-40
US-08-232-081B-40
US-08-127-721A-4
US-08-127-721A-4
US-08-476-176B-8
US-08-476-176B-8
US-08-476-176B-8
US-08-476-176B-8
US-08-476-176B-8
US-08-127-721A-8
US-08-127-721A-8
US-08-127-721A-8
US-08-127-721A-10
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US-09-296-595-8
US-09-510-322A-10
US-09-195-868-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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25
1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 200000000
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Match Length
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Perfect score:
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Maximum DB seq
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Sequence 28, Appl Sequence 90, Appl Sequence 9, Appli Sequence 3, Appli Sequence 1776, Appli Sequence 1776, Appli Sequence 19, Appli Sequence 19, Appl Sequence 110, Appl Sequence 110, Appl Sequence 110, Appl Sequence 11, Appli Sequence 12, Appli Sequence 13, Appl Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 42, Appli Sequence 42, Appli Sequence 82, Appli Sequence 82, Appli Sequence 82, Appli Sequence 82, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA.
COUNTRY: USA
ZIP. 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAR
US-09-195-868-28
US-08-476-3494-90
US-08-476-3494-90
US-08-29-939-3
US-09-244-369B-1
US-09-540-236-3776
US-09-543-681A-6300
US-09-543-681A-6300
US-09-66-281B-19
US-09-468-433C-19
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-42
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illarity 100.0%; Pred. No. 3e+05;
Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIR
STREET: PO BOX 747
CONTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REFERENCE/DOCKET NUMBER: 20-3484
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
     7 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 7 amino a TYPE: amino acid STRANDEDNESS: not
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US-08-127-721A-54

US-08-127-721A-54

Sequence 54, Application US/08127721A

Sequence 54, Application US/08127721A

Sequence 54, Application US/08127721A

GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6066718artis Patent and Trademark Department
STREET: 59 ROUTE 10

CITY: East Hanover
                                                                                        GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                     ADDRESSE: No. 5958708artis Patent Department STREET: 59 Route 10 CITY: Bast Hanover STATE: New Jersey COUNTRY: USA ZIP: USA ZIP: O'936-1080 COMPUTER READABLE FORM: WIDTHW TYPE: Ploppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/POCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPRAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                         Sequence 54, Application US/08476176B Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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Best Local Similarity
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RESULT 2
US-08-476-176B-54
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STATE: New Jersey

COUNTRY: USA

PELLOATION NUMBER: BC. DOS/NS-DOS

FILLAND DATE: AS-SETFERSH-1993

FILLAND TO FILLAND CATAIN DATE: AS-SETFERSH-1993

FILLAND CATAIN DATE: AS-SETFERSH-1993

FILLAND D
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4-19276/A/P2/CIP

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Sequence 4, Application US/08800198
| Patent No. 5942602
| GENERAL INFORMATION:
| APPLICANT: WILLS, WINFRIED S. |
| APPLICANT: SCHWILDS, WARALOPOULOU, EVANGELIA APPLICANT: SCHNEIDER, DOUGLAS |
| TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES |
| NUMBER OF SEQUENCES: 17 |
| CORRESPONDENCE ADDRESS: | MILLEN, WHITE, ZELANO & BRANIGAN, P.C. |
| STREET: 2200 CLARENDON BLVD. SUITE 1400 |
| CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
COUNTRY: US
ZIP: 22201

ZIP: 22201

COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-197
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIAMA
REGISTRATION NUMBER: 33,302
REFERENCE/MOUNTCATION NUMBER: SCH 1576
TELEPHONE: 703-243-6333
TELEPHONE: 703-243-6333
TELEPHONE: TO3-243-6333
TELEFAX: 703-243-6333
TELEFAX: 703-243-6410
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Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE:
US-08-800-198-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 3; Length 99; Best Local Similarity 100.0%; Pred. No. 23; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: WILLIAMS MDPHD, LEWIS T.
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORION STREET
STRIET: ENERYVILLE
STRIET: GUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94608

ZIP: 94608

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/195,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
TATORNEY/AGENT INFORMATION:
NAME: FIRESTONE, LEIGH H.
REFERENCE/DOCKET NUMBER: 182.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-623-2707
TELEPHONE: 510-65-3542
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/09195868 Patent No. 6090621
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEPRAX: (908) 277-5110
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-485-246A-54
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASESIS 7
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USA
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ö Gaps .; 0 ; Score 25; DB 2; Length 106; ; Pred. No. 25; 0; Mismatches 0; Indels Sequence 4, Application US/09296595A

Patent No. 6129915

GENERAL INFORMATION:
APPLICANT: WINELED S.
APPLICANT: SCHMIDT, WATHIAS
APPLICANT: SCHMIDT, WATHIAS
APPLICANT: SCHMIDT, WATHIAS
TILLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
TILLE REPERENCE: SCH-1576 D1
CURRENT APPLICATION UNMERR: US/09/296,595A
CURRENT FILING DATE: 1999-04-23
SEALLER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18 NAKATANI, TOMOYUKI

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                                                                                                                                         100.0%; Score 25; DB 3; Length 106; 100.0%; Pred. No. 25; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NAKATHIN: TOMOYUKI
APPLICANT: MIDENES, JOHN
APPLICANT: MIDENES, JOHN
APPLICANT: MIDENES, JOHN
TITLE OF INVENTION: HIROSHI
TITLE OF INVENTION: HAANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
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Patent No. 5886152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08232081B Patent No. 5886152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SYENSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REPRENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 107 amino acids
amino acid
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 106
                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
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                                                                ; TYPE: PRT
; ORGANISM: Murine sp
US-09-296-595-4
                                                                                                                                                                                                                                                                          51 ASESIS 56
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                                                                                                                                                                                                                                  1 ASESIS 6
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US-08-232-081B-9
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APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: Bast Hanover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                COUNTRY: FALLS CHORCH
COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REFERENCE/DOCKET NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELEFONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
APPLICANT: GOMI, HIDEYUAL
APPLICANT: MIJDENES, JOHN
APPLICANT: MIJDENES, JOHN
APPLICANT: WOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-232-081B-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ASESIS 56
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TOPOLOGY:
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Query Match
Best Local Similarity 100.
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                                                                                                                                                      1 ASESIS 6
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                                                                                                                                                                                                                                                                                                                                     US-08-485-246A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-485-246A-4
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GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
ADDRESSE: SS
CORRESPONDENCE ADDRESS:
ADDRESSE: SP Route 10
CORRESPONDENCE ADDRESS:
ADDRESSE: SP Route 10
CONFEST: SP Route 10
CONFUTE: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: O'36-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATE:
TILNG DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6066718ak, Henry P.
REDERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TO TATA-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 2; Length 107; 100.0%; Pred. No. 25;
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0
                   APPLICATION NUMBER: 08/127,721
PILING DATE: 2-SEPTEMBER-1993
APPLICATION NUMBER: 08/7952,802
FILING DATE: 2-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708Ak, Henry P.
REGISTATION NUMBER: 33,200
REGISTATION NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEFAN: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08127721A Patent No. 6066718 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-476-176B-4
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MOLECULE TYPE: protein

US-08-127-721A-4
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hardman, No. 6072035man
APPLICANT: Kobinger, Frank
APPLICANT: Saldanha, Jose
IIILE OF INVENTION: Reshaped monoclonal antibodies against an
ITILE OF INVENTION: Immunoglobulin isotype
CORRESPONDENCE ADDRESS: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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100.0%; Score 25; DB 3; Length 107; 100.0%; Pred. No. 25;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 6072035artis Patent Department STREET: 59 Route 10
CITY: East Hanover STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: NO. 6072035AK, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMOUTICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASCIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
                                                                                                                                                                                                                                                                    Sequence 4, Application US/08485246A Patent No. 6072035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/08476176B; Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: immunoglobulin isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                            TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
UNMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 2; Length 127; 100.0%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTAY: USA
ZIP: 07936-1080
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAREMENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   ADDRESSE: No. 5958708artis Patent Department STREET: 59 Route 10
CITY: East Hanover STATE: New Jersey
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 25-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORING DATE: 35-SEPTEMBER-1992
ATTORING DATE: 35-SEPTEMBER-1992
ATTORING DATE: 37-SEPTEMBER-1992
ATTORING NUMBER: 33,200
REGISTRATION NUMBER: 33,200
RECISTRATION NUMBER: 33,200
RECISTRATION NUMBER: 32,500
RECISTRATION NUMBER: 327-510
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
TELEPHONE: SEQUENCE CHARACTERISTICS:
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Mismatches
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Best Local Similarity 100.0%;
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TYPE: amino acid
TOPOLOGY: linear
Saldanha, Jose
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Gaps
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Patent No. 5958708
Patent No. 5958708
PAPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 2; Length 127; 100.0%; Pred. No. 31;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
CTATE: Now JETSEY
COUNTRY: USA
                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708AK, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 44-19276/A/P2/CIP
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
TELEPAK: (908) 277-510
TELEPAK: (908) 277-510
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER: 1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER: 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REGISTRATION NUMBER: 33,200
REGISTRATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
APPLICATION NUMBER: US/08/476,176B
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DK
SOFTWARE: Patentin Release #1
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 127 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv.
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-476-1768-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 ASESIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASESIS 6
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| IENGTH: 127 amino acids | TYPE: amino acid |
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Wede from J. Goldstein ?

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5.1.6	Compugen
version	- 2004
GenCore	1993
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OM protein - protein search, using sw model

October 6, 2004, 16:20:48 ; Search time 30.3158 Seconds (without alignments) 55.921 Million cell updates/sec Run on:

US-09-635-974A-10 25 1 ASESIS 6

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04:* 1: geneseqp1980s:*

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* geneseqp1990s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Aay59315 Light cha		Aau77788 Mouse lig	m	-4	4	Aau72852 Anti-NKG2	09		Aag18882 Zea mays	-	ī	_	σι	0 B-B10	a	0	9 Kappa li	18 Kappa	79	04 Vkap	5		6010	Abb80270 Vitaxin l
SUMMARIES	Q		AAY59315	AAB37956	AAU77788	AAR37603	AAY26991	AAU72844	AAU72852	ABB79660	ABB79661	AAG18882	AAG18881	AAW26795	AAW71241	AAR32129	AAR37610	AAR37612	AAR50190	AAW08949	AAW08948	AAY26979	AAY70604	AAU72842	AAU72850	501	ABB80270
•	_ B	: :	m	4	n	N	(7)	rU	ιn	Ŋ	Ŋ	ო	m	0	N	7	0	0	0	7	~	(7	m	ıO	w	φ	7
	Query Match Length DB		9	φ	9	7	7	7	7	61	61	82	83	104	106	107	107	107	107	107	107	107	107	101	107	107	107
de	Query		100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0		100.0		100.0	100.0
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	Result No.	1	1	C/I	٣	4	ľ	9	7	σ	o.	10	11	12	13	14	15	16					21				

Add13784 vKanna ex		Aar50192 Light cha					Aaw08946 Kappa lig	Kappa	Aay26981 Light cha	Light	Aay26982 Light cha	Aao30379 Rabbit 20	Abp96757 ISH recep	Abp96766 TSH recep	Abp96758 TSH recep	Abp96765 TSH recep		Aaw26625 Signallin	Aar34511 Fv(TU25).
ADD13784	AAP90479	AAR50192	AAR50187	AAR50191	AAW08945	AAW08941	AAW08946	AAW08943	AAY26981	AAY26980	AAY26982	AAO30379	ABP96757	ABP96766	ABP96758	ABP96765	ADC79230	AAW26625	AAR34511
7 611	126 1	127 2																	239 2
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3.5	2 1	25																	
Ċ	27	28			31					36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Hypervariable region, complementarity determining region, CDR, tumour, single chain antibody, growth inhibitor, human, tumourigenesis, therapy, protein receptor tyrosine kinase, light chain. Light chain hypervariable region, CDR2. AAY59315 standard; peptide; 6 AA. (first entry) 07-MAR-2000 AAY59315; 

Mus sp.

WO9960023-A1.

25-NOV-1999.

99WO-US010741. 14-MAY-1999;

98US-00079612. 98US-0085613P. 98US-00206138. 15-MAY-1998; 15-MAY-1998; 07-DEC-1998;

(IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND.

Robert F, Buchsbaum DJ; Waksal HW, Saleh MN,

Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor. WPI; 2000-062440/05. N-PSDB; AAZ48629.

Disclosure; Page 15; 31pp; English.

This sequence is the hypervariable region CDR2 (complementarity determining region 2) of the light chain of a single chain antibody deterived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (RRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kichey, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to

the patient makes the tumour more susceptible to radiotherapy

SXC

Matches

AAB37956 ID AAB3 RESULT 2

1 ASESIS

Local Similarity

Query Match

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Gaps

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Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; light chain; antibody; hyperproliferative disease; epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR2; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                            Mouse light chain hypervariable region (CDR2) of 225 antibody.
                                                                                                                                                                                                         AAU77788 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001; 2001WO-US041647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2000; 2000US-00635974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                           (first entry)
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ASESIS 6
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                                                                                                                                                                                                                                                                                                                                           05-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-EGFR monoclonal antibody L chain V region CDR2 peptide sequence.
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                                                                                                                                 100.0%; Score 25; DB 3; Length 6; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB37956 standard; protein; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                      6; Conservative
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                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          1 ASESIS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200069459-A1.
                                                                    Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1999;
13-AUG-1999;
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Mus sp.

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                                                           This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGP) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the rantagonist and phototherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal prosphorylation. The method of the invention is useful for treating a mammal with hyperpoliferative disease such as positissis, actinic keratoses, seborrheic keratoses, warts, keloid scars and eczema stimulated by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 25s antibody light chain (LH) hypervariable region (CDR2) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0;
Disclosure; Page 12; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR37603 standard; peptide; 7 AA.
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AAR37603
ID AAR3
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The invention relates to a method of determining IgE levels in a body full d sample, by contexting the sample with a reshaped human monoclonal antibody (RA) having a binding affinity about equal to that of the murine CDR-donor antibody TES-C21 produced by the cell line 11133. The antibodies are useful in the diagnosis, prophylaxis and treatment of allergy. This sequence represents the complementarity determining region (CDR) 2 from the light chain variable domain of a reshaped human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, NKG2D, NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; mysloma; karcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; 1182D10; 6H7B7; 8G7C10; 6ESA7; 1182D10; 47; 635A724-7; 8G7C10; 655A74-7; 8G7C10; 655A74-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
    binding affinity; mouse; CDR; complementarity determining region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-NKG2D hybridoma 8G7C10 variable light chain CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  new method for determining IgE levels in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                        Saldanha J, Kolbinger F, Hardman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU72844 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Col 67; 19pp; English
                                                                                                                                                                                                                           95US-00476176.
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                                                                                                                                                                                                                                                                      92US-00952802
93US-00127721
                                                                                                                                                                                                                                                                                                                                   (NOVS ) NOVARTIS CORP.
(TANO-) TANOX BIOSYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-570765/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
                                                                                       Homo sapiens
                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                      25-SEP-1992;
27-SEP-1993;
                                                                                                                                    US5958708-A.
                                                                                                                                                                                 28-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU72844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                              allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAR37599-604 represent the complementarity-determining regions (CDRs) of a humanised antibody (Ab) which binds specifically to human interleukin (IL)-2 receptor (HIL2R). These CDRs were derived from the murine anti-human IL-2 receptor monoclonal Ab (MAD) (CC B-B10 (see also AAQ43242-43). This MAD is antagonistic to the binding of IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human compact the Transport of the binding of the B-B10 (Ab was cloned by PCR and sequenced (see also AAQ43256-32 and AAQ43233-36). A human Ab with high levels of amino acid sequence homology to the human about the Hammon's could writh the B-B10 V region CDR and the framework of this Ab was bound with the B-B10 V region CDR and a part of the framework to design several kinds of the humanised B-B10 V region (see also AAQ43244-45). The CDRA sequence coding this humanised B-B10 was synthesised and a plasmid expressing humanised B-B10 was constructed. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised antibody comprising - CDR region of mouse MAB B-B10 specific for IL-2 receptor useful for treating carcinoma expressing IL-2 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                       Complementarity-determining region, CDR; humanised, antibody; hILL2R; human; incerleukhi, IL-2; receptor; murine; anti-human; Ab; T-cell; monoclonal antibody; B-10; mixed lymphocyte reaction; variable; V; region; PCR; framework; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDR2 domain reshaped human antibody light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wijdenes J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY26991 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 43; 62pp; English.
                                                                                                          hIL2R Ab L chain V region CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMU ) SUMITOMO PHARM CO LTD. (BIOT ) BIOTEST PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                91JP-00323319.
                                            (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INNO-) INNOTHERAPIE LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakatani T, Gomi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-197057/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                              WO9311238-A1
                                                                                                                                                                                                                                                                                                                                                                                                   03-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-1991;
                                                                                                                                                                                                                                                                    Mus musculus
                                          25-MAR-2003
13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                         10-JUN-1993
AAR37603;
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Best Local S
Matches 6
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AAY26991 ID AAYX XX AAY XX AAY DT 24-1 XX DE CDR XX KW Dia

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Gaps

Kischel R;

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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recogniess an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated concious account of the NG2D receptor of an extracellular polymolectide are used for the preparation of a pharmaceutical composition. The cancer may be a tumour of the had and neck, stomach, conditions. The cancer may be a tumour of the had and neck, stomach, cosophagus, colon, liver, intrahepatic bile ducts, pancress, lung, larger are to brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, bladder or brain, or a melanoma, myeloma diseases include multiple clerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent disease multimmune hepatitis. Sequences AUT2820-AAUT2875 represent the NKG2D receptor and the polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahegatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; badder; brain; melanoma; myeloma; Fv sarcoma; lenkaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; llB2D10; 6H7B7; 8G7C10; 6E5A7; llB2D10; 6H7B7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; B10xP4-3; B4-14; P5-15; b5-23; B5-24; B10xP4-14;
                                                                                                                                                                         Multifunctional polypeptides comprising binding sites that specifically recognize extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 100.0%; Score 25; DB 5; Length 7; Similarity 100.0%; Pred. No. 1.40+06; 6; Conservative 0; Mismatches 0; Indels
                                                                             Borschert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-NKG2D hybridoma 6E5A7 variable light chain CDR3.
                                                                             Lutterbuese R,
                                                                                                                                                                                                                                                                         Example 3; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU72852 standard; peptide; 7 AA
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24-MAR-2000; 2000EP-00106467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                             o,
                                                                             Riethmueller
Hofmeister R;
                                                                                                                                     WPI; 2002-055119/07
                                                                                                                                                                                                                                        infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASESIS 6
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                                       (KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171005-A2
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                                                                             Kufer P,
Mayer M,
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recogniess an extracellular group of the NG2D receptor complex and a second domain which functions are a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, cosophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larym, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, proteoza or helminths. The autoimmune diseases include multiple sclerosis, drave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent autoimmune hepatitis. Sequences ANU72820-AANU72875 represent the NKG2D receptor and the polypeptides of the invention
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/label= HC-CDR1
/note= "heavy chain complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "light chain complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "light chain complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "light chain complementarity determining region 3"
                                                                                                                                               Multifunctional polypeptides comprising binding sites that specifically recognize extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                  Kischel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chronic lymphocyte leukaemia specific scFv E1c CDR sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chronic lymphocytic leukaemia; CLL; scFv; antibody; rabbit; complementarity determining region; CDR; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                    Borschert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 5; L
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                    Lutterbuese R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                   Example 3; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB79660 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l. .11
/label= LC-CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12. .18
/label= LC-CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19. .28
/label= LC-CDR3
24-MAR-2000; 2000EP-00106467.
                                                                  Riethmueller G,
Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus.
                                                                                                                                                                                                     Infectious diseases.
                                                                                                                   WPI; 2002-055119/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                    (KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB79660;
                                                                    Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Region
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Gaps

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Oryctolagus cuniculus.

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34. .48
/label= HC-CDR2
/note= "heavy chain complementarity determining region 2"
49. .61
/label= HC-CDR3
/note= "heavy chain complementarity determining region 3"
                                                                                                                                                                                New chronic lymphocytic leukemia cell line (designated CLL-AAT), useful for studying, diagnosing or treating chronic lymphocytic leukemia (CLL) disease, or for identifying agents that are useful in the therapy of CLL
                                                                                                                                                                                                                             Claim 12; Fig 9B; 35pp; English.
                                                                                             10-DEC-2001; 2001WO-US047931.
                                                                                                              08-DEC-2000; 2000US-0254113P.
                                                                                                                               (ALEX-) ALEXION PHARM INC
                                                                                                                                                 Mcwhirter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                 WPI; 2002-599775/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61 AA;
                                                           WO200259280-A2
                                                                             01-AUG-2002
                                                                                                                                                Bowdish KS,
  Region
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The present sequence comprises a summary of the complementarity determining regions (CDRs) of the light chain and heavy chain of the Antibody regions (CDRs) of the light chain and heavy chain of the Antibody regions separating the CDRs in the scFv are not given in the sequence. Rabbit scFv antibodies (see ABB79657-81) for B-CLL-specific cell surface antigens were selected using antibody page display and cell surface panning. The invention provides a CLL line, CLL-AAT, derived from a B-CLL primary line without immortalisation by Epstein-Barr virus. The cell line is used to generate antibodies useful in the diagnosis and/or treatment of CLL. Antibodies derived from recombinant libraries may be selected using CLL-AAT as bait to isolate antibodies on the basis of specificity. Single chain antibodies are of particular use as they remain stable in the cytoplasm and retain intracellular binding activity. The binding of the present scFv antibody to primary human cells and cell ince was determined by whole cell ELISA as follows: CLL (primary humans and CLL-AAT cell line) ++; normal, primary human B lymphocytes, +; non-Hodgkin's lymphoma cell line RL -; Burkitt's lymphoma cell line Ramos, - Hodgkin's lymphoma cell line RL -; Burkitt's lymphoma cell line Ramos, the VL and VH regions of the scFv. The antigen recognised by this scFv was CD23, determined by immunoprecipitation and mass spectrometry 100.0%; Score 25; DB 5; Length 61; 100.0%; Pred. No. 53;

0; Mismatches

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Gaps

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0; Indels

ABB79661 standard; protein; 61 AA. 21-OCT-2002 (first entry) ABB79661; RESULT 9 ABB79661 

Chronic lymphocyte leukaemia specific scrv F2d CDR sequences.

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Gaps

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100.0%; Score 25; DB 5; Length 61; 100.0%; Pred. No. 53; ive 0; Mismatches 0; Indels

6; Conservative

Matches

1 ASESIS 6 ASESIS

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Query Match Best Local Similarity

Chronic lymphocytic leukaemia; CLL; scFv; antibody; rabbit; complementarity determining region; CDR; diagnosis; therapy.

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The present sequence comprises a summary of the complementarity determining regions (CDRs) of the light chain and heavy chain of the chronic lymphocytic leukaemia (CLL) specific rabbit serv antibody F2d.

Antibody regions separating the CDRs in the scrv are not given in the sequence. Rabbit scrv antibodies (see ABB79657-81) for B-CLL-specific cell surface antigens were selected using antibody phage display and cell surface panning. The invention provides a CLL line, CLL-AAT, derived from a B-CLL primary line without immortalisation by Epstein-Barr virus. The creatment of CLL. Antibodies derived from recombinant libraries may be selected using CLL-AAT as bait to isolate antibodies on the basis of specificity. Single chain antibodies are of particular use as they remain specificity. Single chain antibodies are of particular use as they remain specificity. Single chain antibodies are of particular use as they remain school in the present scrv and clubarian and cell lines was determined by whole cell ELISA as follows: CLL (primary tumours and chain such cell lines was determined by whole cell ELISA as follows: CLL (primary tumours and human erythroleukaemia cell line RL, -; Burkitt's lymphoma cell line Ramos, and human erythroleukaemia cell line FP-1, -. A short linker separates
                                                                                                                                                                                                                                                                                                         19. .61
| Tabel= HC-CDR3
| Incte= "heavy chain complementarity determining region 3"
                                                                                              .2. .18
|Tabel= LC-CDR2
|Tote= "light chain complementarity determining region 2"
                                                                                                                                                                                                    14. .48
| Tabel= HC-CDR2
| Incte= "heavy chain complementarity determining region 2"
                                                                                   "light chain complementarity determining region 1"
                                                                                                                                                                                      note= "light chain complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chronic lymphocytic leukemia cell line (designated CLL-AAT), useful for studying, diagnosing or treating chronic lymphocytic leukemia (CLL) disease, or for identifying agents that are useful in the therapy of CLL
                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 9B; 35pp; English.
                                                      label= LC-CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000US-0254113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-2001; 2001WO-US047931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALEX-) ALEXION PHARM INC.
                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-599775/64.
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9905-0139460P

9905-0139463P

9905-0139463P

9905-0139763P

9905-013989P

9905-0140635P

9905-0140635P

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9905-0144884P

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9905-0144331P
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99US-0145276P.
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99US-0147416P.
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99US-0147935P.
99US-0148171P.
99US-0139458P.
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02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
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11-AUG-1999;
12-AUG-1999;
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04-AUG-1999;
05-AUG-1999;
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06-AUG-1999;
06-AUG-1999;
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                                                                                                                                                                                             01-JUL-1999;
                                                                                                                                                                                                                                                                     12-JUL-1999
 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                             Zea mays protein fragment SEQ ID NO: 20468.
                                        AAG18882 standard; protein; 85 AA
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                                                                                        17-OCT-2000 (first entry)
                                                                                                                                                                                        Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                       23-WAR-1999;
25-WAR-1999;
29-WAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
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18-MAY-1999;
19-MAY-1999;
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27-MAY-1999;
28-MAY-1999;
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21-MAY-1999;
24-MAY-1999;
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08-JUN-1999;
10-JUN-1999;
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14-JUN-1999;
16-JUN-1999;
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23-APR-1999;
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30-APR-1999
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                                                               AAG18882;
                  RESULT 10
AAG18882
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                      Zea mays protein fragment SEQ ID NO: 20467.
                                                                                                                                                         990S-01218259.
990S-01231809.
990S-01254889.
990S-01254889.
990S-01267859.
990S-01267859.
990S-01282349.
990S-01382349.
990S-01382349.
990S-01305109.
990S-01305109.
990S-01305109.
990S-01324869.
990S-01342199.
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990S-01394529.
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    (first entry)
                                                                                Zea mays subsp. mays.
   17-OCT-2000
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09-MAR-1999;
25-MAR-1999;
25-MAR-1999;
29-MAR-1999;
06-APR-1999;
06-APR-1999;
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19-APR-1999;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG18881 standard; protein; 89 AA.
99US-0149929P.
99US-0149929P.
99US-0149929P.
99US-0150565P.
99US-0151065P.
99US-0151065P.
99US-0151065P.
99US-0151080P.
99US-0151303P.
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99US-0152363P.
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99US-0161993P.
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                            23 - AUG - 1999;
25 - AUG - 1999;
27 - AUG - 1999;
27 - AUG - 1999;
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31 - AUG - 1999;
31 - AUG - 1999;
31 - AUG - 1999;
32 - SEP - 1999;
33 - AUG - 1999;
34 - SEP - 1999;
35 - SEP - 1999;
36 - AUG - 1999;
37 - AUG - 1999;
38 - AUG - 1999;
39 - AUG - 1999;
30 - AUG - 1999;
31 - AUG - 1999;
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AC AAG1
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99US-0139763P.

18-JUN-1999

21-JUN-1999) 22-JUN-1999) 23-JUN-1999) 23-JUN-1999) 24-JUN-1999)

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Single chain antibody; scFv; monoclonal antibody; MAb; 48-127; trop-2; gp54; antigen; cancer marker; bladder cancer; breast cancer; cervix cancer; prostate cancer; metastasis; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 8
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                                              9905-0151303P

9905-0151303P

9905-01513070P

9905-0153070P

9905-0153070P

9905-0154039P

9905-0154039P

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9905-0155458P

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9905-015929P

9905-015929P

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9905-015929P

9905-015929P

9905-01609P

9905-01609P
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99US-016136DP.
99US-016136DP.
99US-0161992P.
99US-0161932P.
99US-0162142P.
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Matches 6; Conserv
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24.5EP-1999;
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24.5EP-1999;
26.5EP-1999;
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26.5EP-1999;
26.5EP-1999;
26.5EP-1999;
27.5EP-1999;
28.5EP-1999;
28.5E
                                              30-AUG-1999;
31-AUG-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
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29-OCT-1999;
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ID AAW2
XX
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KW Sing
KW GP54
KW Gery
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99US-0142803P.
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99US-014332P.
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18-AUG-1999; 20-AUG-1999; 20-AUG-1999;

16-AUG-1999

03-AUG-1999; 04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 09-AUG-1999; 09-AUG-1999;

11-AUG-1999; 12-AUG-1999; 13-AUG-1999;

Mus sp Region Region Region

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The present sequence represents the light chain variable domain of murine monoclonal antibody 14E1. This antibody is active against the human epidermal growth factor receptor (EGF-R). The sequence is used to construct a single-chain polygeptide (scFv) that has binding affinity for an EGF-R. The scFv comprises two segments which contain the binding parts of the heavy and light chain variable domains of the monoclonal antibody 14E1. The scFvs of the invention are used to treat carcinomas (gliomas, melanomas and tumours) that overexpress EGF-R, specifically EGF-RVIII, relative to normal cells, particularly by blocking proliferation of such vitro purging. When the scFv is approxiately labelled, it can be used diagnostically to image cells that express EGF-R, specifically breast
                                                                                                                                                                                                                                                                                                             New single chain polypeptide that binds to epidermal growth factor receptor - is derived from antibody 14E, used for treatment and diagnosis of cancer or other cell proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppression; tissue transplantation; graft; L chain; V region;
T-helper cell inhibition; transplant rejection; MAb;
interleukin-2 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 2; Length 106; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                   Schneider DW;
                                                                                                                                                                                                                 Vakalopoulou E,
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/label= V-region
97. .107
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/label= J-region
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(revised)
(first entry)
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N-PSDB; AAV54788.
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                      WO9836074-A2
                                                                                             13-FEB-1998;
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02-JUN-1993
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Region
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Matches
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AAR32129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises the light chain variable region of murine monoclonal antibody (MAb) 48-127. This MAb recognises an epitope of gp54 antigen (frop-2), a cancer marker expressed at the surface of bladder, breast, uterine and prostate cancers. MAb 48-127 (IgG1) reacts with a majority of human bladder cell lines and with human breast carcinoma cell lines. The invention relates to novel single chain antibody (scFv) molecules, including a 48-127 scFv (see AAW2679) that comprises the 48-127 VH and VL chains joined via a linker. Such scFvs can be used to detect cancers and micrometastases, e.g. bladder, prostate, breast or uterine cervix cancers, and may be linked to specific toxins for use in cancer therapy. The scFvs are not immunogenic and are distributed and captured by 9P45-bearing target cells more quickly than conventional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant antibodies to gp54 antigen - used for the detection of cancers and metastases and for therapy of cancers expressing the gp54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels
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human epidermal growth factor receptor; EGF-R;
EGF-RvIII; in vitro purging; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Light chain variable domain of antibody 14E1.
                                                                         ocation/Qualifiers
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                                                                                                                                  47. .54
/label= CDR2
76. .84
/label= CDR3
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                                                                                               21. .31
/label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                  (DIAG-) DIAGNOCURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           Fradet Y, Darveau A;
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N-PSDB; AAV26766.
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immunotherapy
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antigen

AAW71241;

RESULT 13

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Mus sp.

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Gaps

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Humanised antibody comprising - CDR region of mouse MAB B-B10 specific for IL-2 receptor useful for treating carcinoma expressing IL-2 receptor

N-PSDB; AAQ43243.

Disclosure, Fig 2; 62pp; English.

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                                                                                                                                                                                                                       This sequence is the light chain variable region of a preferred anti-IL2R beta monoclonal antibody for use in the claimed synergistic composition. The anti-IL2R beta antibody is used with at least one anti-CD4 antibody. Individually the antibody served with inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See AAQ36607-Q36616. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                 Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity-determining region, CDR; humanised, antibody; hIL2R; human; interleukhn; IL-2; receptor; mutine; anti-human; Ab; T-cell; monoclonal antibody; B-l0; mixed lymphocyte reaction; variable; V; region; PCR; framework; plasmid; heavy; H; light; L.
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                                                                                             Riethmueller G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR37610 standard; protein; 107 AA.
                                                                                             Scheuer W, Kaluza B,
                                                                     (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                    Claim 8; Page 17; 18pp; German.
                       91DE-04143214
                                               91DE-04124759
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(first entry)
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N-PSDB; AAQ36615.
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                                                                                                                                                                                                                                                                                                                                                 Sequence 107 AA;
                       30-DEC-1991;
                                               25-JUL-1991;
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13-OCT-1993
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 28-JAN-1993
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Wijdenes J, Noguchi H;

Gomi H,

Nakatani T,

WPI; 1993-197057/24

91JP-00323319.

06-DEC-1991;

92WO-JP001583

03-DEC-1992;

(SUMU ) SUMITOMO PHARM CO LID. (BIOT ) BIOTEST PHARMA GMBH.

(INNO-) INNOTHERAPIE LAB.

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The sequences given in AAR37609-10 represent the heavy (H) and light (L) chain variable (V) regions of the murine anti-human IL-2 receptor monoclonal antibody (MAD) B-10, respectively. This MAD was used in the construction of a humanised antibody (AD) which binds specifically to human interleukin (IL)-2 receptor (HIL2R). The complementarity-catemining regions (CDRs) for the hIL2R MAD were derived from B-110 (see also AAR37599-04). The hIL2R MAD is antagonistic to the binding of IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human mixed lymphocyte reaction. The CDNA encoding the variable (V) region of ILe B-10 W pass cloned by PCR and sequence (see also AAQ43226-32 and AAQ43233-36) A human AD with high levels of amino acid sequence homology to the murine sequence was selected and the framework of this AD was bound with this sequence was selected and the framework of this AD was bound with thinds of the humanised B-10 V region. The DNA sequence coding this humanised B-10 W as synthesised and a plasmid expressing humanised B-10 was synthesised and a plasmid expressing humanised B-10 was constructed. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                 141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                            KV09 RABIT
KV51 MOUSE
PGL1_ASPNG
ENGA_STRAW
CNGA_STRAW
CNGA_STRAW
X1J0_YEAST
SYT_CHLMU
BOSS_BROVI
IGA_NEIGO
Y007_CHLTR
MGBI_HUMAN
LMRA_LACLA
HSCA_SALTI
HSCA_SALTI
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Maximum Match 100%
Listing first 45 summaries
                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                  US-09-635-974A-10
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Maximum DB seq length: 200000000
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Query
Match Length DB
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                                                                                   Title:
Perfect score:
                                                                                                                      Scoring table:
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                                                                                                     Sequence:
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                                                 Run on:
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ASPG PSEFL GDN MOUSE YM42 MYCTU YCCE ECOLI ARP3 SCHPO CLPX CLOAB HISX ECOL6 HISX ECOL6 HISX ECOL1 HISX ECOL1 HISX ECOL1 YGDV SCOL1 ARSY SCOL1 ALIGNMENTS	SULT 1  KV09_RABIT  KV09_RABIT  STANDARD; PRT; 92 AA. P01650, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1996 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V region 3381 (Fragment). Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertek Mammalia; Butheria; Lagomorpha; Leporidae; Ory NCBI_TAXID=9986; [1] SEQUENCE. MEDLINE=75176905; PubMed=1094456; MEDLINE=75176905; PubMed=1094456;	"Diversity of light chain variable regions sequent antibodies elicited by the same antigens."; Proc. Natl. Acad. Sci. U.S. A. 72:2180-2184 (1375) -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM. PRIMOCOCCI AND WAS ISOLATED FROM THE SERUM (HSSP, PO1607, 1REI. INTERFRO, IRRON110; 1g-1ike. InterPro; IRRON3596; 1g-v. Pfam, PF00047; ig; 1. SMART; SMO0406; IGV; 1. IRRON1TE; PS5035; IG LIKE; 1. Immunoglobulin V region. IRRAMEWORK-1. ITAMEMORIAN 1 23 COMPLEMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY-DETTERMENTARITY	FRAMEWORK-2. COMPLEMENTARITY- COMPLEMENTARITY- SASGES SON STATE SCORE 25, DB 1 Pred. NO: 4.9,		SE STANDARD; PRT; 115 AA.  86 (Rel. 01, Created)  86 (Rel. 01, Last sequence update)  973 (Rel. 42, Last annotation update)  974 Mouse).
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	1 1 KNO9 RABIT KNO9 RABIT PO1650. 21-JUL-198 21-JUL-198 21-JUL-199 COTYCTOLOGU EUKARYOCA; MAMMALIA; [1] [1] [1] SEQUENCE:	"Diversity of light chanticodes elicited by Proc. Natl. Acad. Sci. 1- MISCELLANGOUS: THI PREUMOCOCI AND WARPER, A01953; KWRB8. HSSP, PO1607; IREI. InterPro; IPRO07110; InterPro; IPRO07110; InterPro; IPRO0710; IPRO0715; SMART, SMO407; ig. 1. PROSITE; PSS0835; IG. IRMUNOGIODULIN V region DOMAIN 24 3 3 4	Sal Car	, H 12	E MOUS 42; UL-19 UL-19 CT-20 appa
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EMBL; AL939110; CAC12931.1; ALT_INIT.
HAMAP; MF_00195; -; 1.
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STRAIN=A3(2) / M145;
                                                                                                                                                                     368 AA;
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                            43 ASESIS 48
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                                   SEQUENCE FROM N.A.
MEDLINE=81220975; PubMed=6264318;
Pech M., Hochtl J., Schnell H., Zachau H.G.;
"Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:668-670(1981).
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

NCBI_TaxID=5061;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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2, Last annotation update)
precursor (EC 3.2.1.15) (PG-I) (Pectinase)
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                          115
12615 MW; C17BEC758C577E00 CRC64;
                                                                                                                        PDB; 1010; 18-FEB-03.
PDB; 1017; 18-FEB-03.
PDB; 1017; 18-FEB-03.
InterPro; 1PR00710; 1g-1ike.
InterPro; 1PR0045; 1g, 1.
SMAR; SMO467; 1g; 1.
FROSITE; PS50835; 1G_LIKE; 1.
FROSITE; PS50835; 1G_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      368 AA
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115 1
115 AA;
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                   NCBI TaxID=10090;
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P26213;
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SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             EMBL; X58892; CAA41693.1; -.
PIR; S17980; S17980.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR0006526; PbHI.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SW00710; PbHI.; 6.
PROSTIF; PS00502; POLYGALACTURONASE; 1.
Hydrolase; Glycosidase; Cell wall; Signal; Zymogen; Multigene family; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome sequence of the model actinomycete Streptomyces
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N-LINKED (GLCNAC. . .) (PROBABLE)
CD9846A9A99B5102 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 1; Length 368; 100.0%; Pred. No. 23; 0; Indels iive 0; Mismatches 0; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
GTP-binding protein engA.
Streptomyces coelicolor:
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31 PO
368 PO
229 PR
246 N-
38108 MW;
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Nature 417:141-147(2002).
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AP005047;
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COG3 HUMAN
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           DARAGO RANGE RANGE
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STRAINEMA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

STRAINEMA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE-21477403; Pubmed=11572948;

Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,

Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 1; Length 465; 100.0%; Pred. No. 30; ive 0; Mismatches 0; Indel8
                      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
GTP-binding protein enga.
ENGA OR SAV6524.
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GTP-bindding_dom.
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Best Local Similarity 100.
Matches 6; Conservative
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MEDLINE=22050606; PubMed=11929878;

MEDLINE=22050606; PubMed=11929878;

Loh E., Hong W.;

Toolgi and exists in a complex with GTC-90 and IdlBp.";

J. Sec34 is implicated in traffic from the endoplasmic reticulum to the conjugated in Endology and IdlBp.";

J. Biol. Chem. 277:21955-221961(2002).

J. Biol. Chem. 277:21955-221961(2002).

J. Biol. Chem. 277:21955-221961(2002).

J. SUBCINIT: Component of the conserved oligomeric Golgi complex which conjugated in ER-Golgi transport.

J. SUBCINIT: Component of the conserved oligomeric Golgi complex which conjugated morphology and localization (By similarity).

J. SUBCELLULAR LOCATION: Golgi. Associated with the peripheral membrane of cisfmedial cisternae.

T. SUBCELLULAR LOCATION: Golgi Associated with highest levels in pancreas and testis and lowest levels in lung.

J. SIMILARITY: Belongs to the COG3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21303883; PubMed=11292827; Suvorova E.S., Kurten R.C., Lupashin V.V.; Judentification of a human ortholog of Sec34p as a component of the cis-Golgi vesicle tethering machinery."; J. Biol. Chem. 276:22810-22818 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
20-FBB-2003 (Rel. 41, Last annotation update)
20-FBB-2003 (Rel. 41, Last complex component 3 (Vesicle docking protein SEC34 homolog) (p94).
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GTP 1 (POT
GTP 1 (POT
GTP 2 (POT
GTP 2 (POT
GTP 2 (POT
HAMAP; MF 00195; -; 1.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR005289; GTP-bindding_dom.
                                                                                             InterProj 1PR005293 GIT-LIMIGALING—GO
InterProj 1PR005217; MRM. HSR1.
InterProj 1PR005255, Small GTP.
PERM: PP01926; MRM. HSR1, 1.
PRINTS: PR00326; GTP10BG.
SWART: SM00382; GTP10BG.
IIGRPAMS; TIGR00569; MG442; 2.
TIGRPAMS; TIGR00531; Small GTP; 2.
GTP-binding; Repeat; Complete Proteon
NP_BIND 168 110 GTP 1 (NP_BIND 188 110 GTP 2 (NP_BIND 188 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 ASESIS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal brain;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S286 / AB972;
STRAIN-S286 / AB972;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Noule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
Withe nucleotide sequence of Saccharomyces cerevisiae chromsome IX.";
Wature 387:84-87(1997).
                                                                                                                                                                                           MALT, 1,730.9.

GO; GO:0005768; C:endosome; TAS.

GO; GO:000582; C:intermediate filament; TAS.

GO; GO:000582; C:intermediate filament; TAS.

GO; GO:0006893; E:microtubule cytoskeleton; TAS.

GO; GO:0006893; E:microtubule binding; TAS.

GO; GO:0006893; E:microtubule binding; TAS.

InterPro; IPR000938; CAP-GIY.

InterPro; IPR001976; Znf CCHC.

PRART; SM0343; Znf C2HC; 1.

PROSITE; PS00845; CAP GIY, 2.

Cytoskeleton; Microtubule; Coiled coil; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomyoota; Saccharomyootina; Saccharomyoetes;
Saccharomyoetales; Saccharomyoetaceae; Saccharomyoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypochetical 56.3 kDa protein in SGAl-KTR7 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 1427; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1408 1421 CCHC-BOX.

457 491 Missing (in isoform Short).

//TIGL=VSP 000765.

1069 D -> E (IN REF. 2).

1427 AA, 160989 MW; 0A4F166DD94254E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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SER.RICH.
CAP-GLY 2.
SER.RICH.
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%; P. Conservative 0;
                                                                        EMBL; X64838; CAA46050.1; -.
EMBL; M97601; AAA35693.1; -.
PIK; S22695, S22895.
Genew; HGNN:10461; RSN.
MIM; 179838; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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ID YIJO YEAST
NC P40499;
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DOMAIN
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             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Isoid=130622-2; Sequence=VSP 000765;
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
OF HODGKIN'S DISEASE.
OF HODGKIN'S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Peripheral blood monocytes;
MEDLINE=92289675; PubMed=1600942;
Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M.,
Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W.,
de Wolf-Peeters C., Shipman R.;
"Restin: a novel intermediate filament-associated protein highly
expressed in the Reed-Sternberg cells of Hodgkin's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-PBB-2003 (Rel. 41, Last annotation update)
Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-sternberg intermediate filament associated protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0
                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 1; Length 828; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                         Genew, HGNC...

MIM; 606975; --
Interpro; IPR007265; Sec34.
Pfan; PF04136; Sec34; 1.
Transport; Protein transport; Golgi stack; Membrane.
Transport; Protein transport; HE -> QQ (IN REF. 2).
CONFLICT 106 107 HE -> QQ (IN REF. 2).
747 N -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                         entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                  EMBL; AF349676; AAK66974.1; -.
                                                                                                                                    EMBL; AF332595; AAK06848.1; -. Genew; HGNC:18619; COG3.
                                                                                                                                                                                                                                                                                                                                                                                      100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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DJ 1907 28-FEB-
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MEDLINE=20150255; PubMed=10684935;

MEDLINE=20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

A Minter C., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

Eisen J., Fraser C.M.,

Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

Eisen J., Praser C.M.,

Mucleic Acids Res. 28:1397-1406(2000).

I. Nucleic Acids Res. 28:1397-1406(2000).

I. OATALTYTC ACTIVITY: ATP + L-threonine + tRNA(Thr) = AMP +

diphosophate + L-threonyl-trRNA(Thr).

C. - CAPACTOR: Binds 1 zinc ion per subunit (By similarity).

C. - COFACTOR: Binds 1 zinc ion per subunit (By similarity).

C. - SUBULIT: Homodaimer (By similarity).

C. - SUBULIT: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.0%; Score 24; DB 1; Length 491; 83.3%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  BAEC655534E04239 CRC64;
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send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                     56332 MW;
                                       EMBL; Z46728; CAA86704.1; -. PIR; S49790; S49790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                              GermOnline, 139625, -.
SGD, S0001352, YIL090W.
Hypothetical protein, T
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HSSP; P00955; 1EVL.
TIGR; TC0870; -.
HAMAP; MF_00184; -; 1.
                                                                                                                                             protein;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  491 AA;
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InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004055; TGS dow.
InterPro; IPR002320; TRNA-SYNT 2b.
InterPro; IPR002320; TRNA-SYNT 2b.
InterPro; IPR005129; TRNA-Igase_II.
Pfam; PF03129; HGTP, anticodon; 1.
Pfam; PF03129; HGTP, anticodon; 1.
Pfam; PF03129; TRNA-SYNT 2b; I.
Pfam; PF05804; TGS; TRNASYNTHTR.
TIGRFAMS; TIGR00418; thrS; I.
TIGRFAMS; TIGR00418; thrS; I.
Aminoacyl-ERNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Aminoacyl-ERNA synthetase; Protecome.
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(BY SIMILARITY).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Phydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%; Score 24; DB 1; Length 635; 83.3%; Pred. No. 82; 1; Mismatches 0; Indels
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SIGNAL
1 30 POTENTIAL.
CHAIN 31 899 ERIDE OF SEVENLESS PROTEIN.
DOMAIN 32 530 EXTRACELLULAR (POTENTIAL).
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ZINC (CATALYTIC) (BY SIMII
ZINC (CATALYTIC) (BY SIMII
; 39825894E70521AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Bride of sevenless protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, L08132, AAA72332.1; -.
PIR, A47550, A47550.
FlyBase, FBgn0013105, Dvir\boss.
InterPro, IPR002956; Bride of 7less.
InterPro, IPR000337, GPCR Mgr.
PF000033, 7tm_3:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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568 ASESVS 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87115823; PubMed=3027577;
Pohlner J., Halter R., Beyreuther K., Meyer T.F.;
"Gene structure and extracellular secretion of Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=90154052; PubMed=2105953;
Bachovchin W.W., Plaut A.G., Flentke G.R., Lynch M., Kettner C.A.;
Inhibition of IgAl proteinlases from Neisseria gonorrhoeae and
Hemophilus influenzae by peptide prolyl boronic acids.";
J. Biol. Chem. 265:3738-3743(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 265:3738-3743(1990).
-!- FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.
-!- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
IgA-specific serine endopeptidase precursor (EC 3.4.21.72) (IgA
                                                                                                                                 N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                     (POTENTIAL)
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Bacteria; Próteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                               Score 24; DB 1; Length 893;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                       99939 MW; ABB9D4C21DB680C3 CRC64;
                                                                                                         (POTENTIAL)
                                                                                                       CYTOPLASMIC (POTENTIAL N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                 PRT; 1532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN=MS11;
                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                       POTENTIAL.
 POTENTIAL
                            POTENTIAL
                                         POTENTIAL
                                                                                                                                                                                                                96.0%;
83.3%;
                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 325:458-462(1987)
                          627
650
673
712
742
772
772
893
307
                                                                                                                                                                                                                                                                                              676 ASESVS 681
                                                                                                                                                                                       893 AA;
                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                     1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgA protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                              IGA NEIGO
P09790;
                                                                                                                                                                                                                                                                                                                                                                                                                                              protease).
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CARBOHYD
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SEQUENCE
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MEDLLNE=99000809; PubMed=9784136;
Stephens R.S., Kaman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Aitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 282:754-759(1998).
-!- SIMILARITY: Belongs to the chlamydial CPn0441/CT007/TC0275 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGA-SPECIFIC SERINE ENDOPEPTIDASE. HELPER PEPTIDE. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00921; IGASERPTASE.
TYGRRAM; TIGR01414; autotrans barl; 1.
Hydrolase; Serine protease; Zymogen; Autocatalytic cleavage;
Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 1; Length 1532;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 CLEAVAGE (AUTO-).
CLEAVAGE (AUTO-).
22 CLEAVAGE (AUTO-).
168976 MW, 68FF4112BD22F40D CRC64;
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PIR: B11569, B11569.
Hypothetical protein; Complete proteome.
Hypothory 316 AA, 35637 MW, 904D2CC28F5CB06E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                               InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
InterPro; IPR009003; Cye Ser_Lrypsin.
InterPro; IPR0001010; Peptidase_S6.
InterPro; IPR0004899; Pertactin.
InterPro; IPR000844; TryBF.
Fam; PF03797; Autotransporter; 1.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.0%;
83.3%;
EMBL; X04835; CAA28538.1; -.
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CT007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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1532 AA;
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                               PIR; A26039; A26039.
MEROPS; S06,001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Chlam
NCBI_TaxID=813;
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O84010;
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SEQUENCE
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PROPEP
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   DORRANDOR STATE OF THE SOLUTION OF THE SOLUTIO
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Score 23; DB 1; Length 316; Pred. No. 73;

92.0%;

Query Match Best Local Similarity

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Proc. Natl. Acad. Sci. Us. S.A., 99:16899-16903(202).

1 TISSUES SPECIFICITY: Expressed in testis and in liver cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Hepatoma;
MEDLINE=22092308; PubMed=12097419;
MEDLINE=22092308; PubMed=12097419;
Wang Y., Han K.-J., Pang X.-W.; Vaughan H.A., Qu W., Dong X.-Y.,
Wang Y., Han K.-J., Pang X.-W.; Leng X.-S., Cebon J., Burgess A.W.,
Peng J.-R., Zhao H.-T., Rui J.-A., Leng X.-S., Cebon J., Burgess A.W.,
Chen W.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gure A.O., Stockert E., Arden K.C., Boyer A.D., Viars C.S., Scanlan M.J., Old L.J., Chen Y.-T.; "CT10: a new cancer-testis (CT) antigen homologous to CT7 and the MAGE family, identified by representational difference analysis."; Int. J. Cancer 85:726-732 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20321428; PubMed=10861452;
Lucas S., De Plaen B., Boon T.;
"MAGE-B5, MAGE-C2, and MAGE-C3: four new members of the MAGE
family with tumor-specific expression.";
Int. J. Cancer 87:55-60(2000).
  Gaps
                                                                                                                                                                                 MGEI_HUMAN STANDARD; PRT; 3/3 AA.

909UBFi, OPPLMG; OSPLMY;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Melanoma-associated antigen El (MAGE-El antigen) (MAGE-C2 antigen)
(Hepatoccilia carcinoma-associated antigen 587) (Cancer-testis
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Suteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Large scale identification of human hepatocellular carcinoma-associated antigens by autoantibodies.";
J. Immunol. 169:1102-1109(2002).
  Indels
  ·,
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20164600; PubMed=10699956;
  ;
                                                                                                                                                                                                                                                                                                                                    antigen CT10).
MAGEE1 OR MAGEC2 OR HCA587.
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                             172 ASESLS 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                       1 ASESIS 6
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Matches
                                                                                                                                           RESULT 13
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Multidrug resistance ABC transporter ATP-binding and permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGE.
SER-RICH.
POLY-GLU.
POLY-GLU.
SER-RICH.
M -> T (IN REF. 1; AAP34816).
K -> E (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 88;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=111403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                 EMBL; AF116194; AAF34816.1; --
EMBL; AF116195; AAF34817.1; --
EMBL; AF196483; AAF07211.1; --
EMBL; AF151378; AAF07210.1; --
EMBL; AF151378; AAF36533.1; --
EMBL; AF239802; AAK15073.1; --
EMBL; BC005891; AAH0891.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen, Multigene family.

DOWAIN

DOWAIN

141

34

BOOVAIN

OOVAIN

67

CONFLICT

SEQUENCE

334

SEQUENCE

34

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CONFLICT

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CONFLICT

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377

ANTIGENCE

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PROSITE; PS50838; MAGE;
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Search completed: October 6, 2004, 16:30:30 Job time : 6.68421 secs
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MEDLINE=97008061; PubMed=8855237;
Wan Veen H.W., Venema K., Bolhuis H., Oussenko I., Kok J., Poolman B.,
Driessen A.J., Konings W.N.; Bolhuis H., Oussenko I., Kok J., Poolman B.,
Multidrug reasistance mediated by a bacterial homolog of the human
multidrug reasistance mediated by 33:1068-10672(1996).

- Proc. Natl. Acad. Sci. U.S.A. 93:1068-10672(1996).
-!- FUNCTION: Efflux transporter for a variety of amphiphilic cationic
compounds, including antibiotics.
-!- SUNGNICH Homodimer (Potential).
-!- SUNGNICH Homodimer (Potential).
-!- SUNGNICH LOATION: Integral membrane protein (Probable).
-!- SUNICHELITE: Belongs to the ABC transporter family.
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Bacceria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1359;
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28-FBB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Multidrug resistance ABC transporter ATP-binding and permease
                                                                                                                                         SMART; SM00382; AAA; I.
PROSITE; PS50929; ABC TM1F; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
ATP-binding; Transport; Transmembrane; Antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                          Length 590;
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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POTENTIAL.
ABC TRANSPORTER.
ATP (POTENTIAL).
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send an email to license@isb-sib.ch)
                                                     InterPro; IPR003593; AAA_ATPase.
InterPro; IRR001140; ABC_TM transpt.
InterPro; IPR001409; ABC_TM transpt.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Probon; PD00006; ABC_tran; 1.
SMART; SM00382; AAA; 1.
                         EMBL; AE006305; AAK04809.1; ALT_INIT
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InterPro; IPR003593; AAA_ATPase.
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                     Interpro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; I.
PROSITE; PS50929; ABC_TRIF; 1.
PROSITE; PS5029; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport; Transmembrane; Antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 1; Length 590;
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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InterPro; IPR001140; ABC_TM transpt.
InterPro; IPR003439; ABC_transporter
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Local Similarity 83.3%;
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Quqm5 homo sapien Q8ci04 mus musculu Q8c0s5 mus musculu

Q8dy17 streptococc Q8p3v6 xanthomonas Q8p3v6 xanthomonas Q92656 homo sapien Q92656 homo sapien Q92656 homo sapien Q9145 homo sapien Q9145 homo sapien Q9145 rattus norv Q8473 streptococc Q91x2 rattus norv Q84811 streptococc Q91x23 mus musculu Q92231 mus musculu Q92231 mus peculo Q92403 escherichia Q81800 cyrnebacte Q91x80 cyrnebacte Q91x80 cyrnebacte Q91x90 drosophila Q81999 drosophila Q81999 drosophila Q91x41 dictyosteli Q91x41 dictyosteli

Q8T909 Q8IPW9 Q9VQ15 Q9NKW1 O21860

094462 09U0MS 09U0MS 08U0MS 08DWL7 08BWL7 0912835 0912835 091280 000145 091280 091283 091283 091283 091283 091283 091283 091283 091283 091283 091283 091283 091283 091283

us-09-635-974a-10.rspt

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CSTRAIN=MARP301099;
KA RADEINE-21082930; PubMed=11214968;
KADEINE-21082930; PubMed=11214968;
KADEINE-21082930; PubMed=11214968;
KADEINE-21082930; PubMed=11214968;
KADEINE-21082930; PubMed=11214968;
KADEINE-21082930; PubMed=11214968;
KADEINE-21082930; Rohara A., Kawashima K., Kimura T.,
Kansha Y., Kijokawa C., Kohara M., Matsumoto M., Matsumoto M., Matsumoto A.,
Mochizuki Y., Nakayama S., Rohazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Mochizobium loti.";
DNA Res. 7:331-33812000.

SMEL; AP003005; BABSIS691.;
RHEJ; AP003005; BABSIS691.;
RHEJ; AP001005; BABSIS691.;
RHEJ; AP001005; CSTAA; SIS68 MW; 9149D55CB83A3877 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
HYPOCHERICAL TrEMBLrel. 23, Last annotation update)
MLL5052.
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Q98qq6 mycoplasma
Q99m54 mus musculu
Q88m34 mus musculu
Q88m39 pseudomonas
Q7x6h5 oryza sativ
Q86m4 homo sapien
Q86m3 caenorhabdi
Q82m37 streptomyce
Q82m37 streptomyce
Q92m3 thermoplasm
Q7vdf7 prochloroco
Q7vg1 prochloroco
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                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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MEDINES22354683; PubMed=12466851;
The FANTOW CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Chromosome 6 BAC-284H12 (RESEARCH GENETICS mouse BAC LIBRARY) complete sequence (RESEARCH GENETICS mouse BAC LIBRARY) (2410005A12RIK protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny D., Ansari-Lari M.A., Timms K.M., Yu W., Dugan S., Lu J., Shen Y., Rowland K., Liu W., Perez L., Ding Y., Haywood M., Jain A., Leal B., Logan O., Nguyen V., Savage L., Shen H., Worley K., Chen E., Forcum J., Arenson A.D., Chiu M.W., Gorrell J.H., Brundage E., Di W., "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny D., Arenson A.D., Adams C., Brundage E., Bunac C., Carvelli K., Chacko J., Chen J., Di W., Ding Y., Dugan S., Durbin J., Forcum J., Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M., Hernandez J., Jackson L., Jin S., Kampathy S., Karpathy S., Kovar C., Leal B., Li Y., Lichtarge O., Liu W., Logan O., Lu J., Ly T., Martinez C., Oswal G., Perez L., Rashid N.D., Rowland K., Savage L., Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J., Vo. Williamson A., Worley K.C., Yu W., Chinault C., Nelson D., Gibbs R.A.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98112780; PubMed=9445485;
Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                              "Comparative sequence analysis of a gene-rich cluster at human chromosome 12p13 and its syntenic region in mouse chromosome 6."; Genome Res. 8:29-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                      (Gene rich cluster).
GRCC8 OR C8 OR 2410005A12RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                      Lu J., Gorr
Gibbs R.A.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                          STRAIN-UAB CTIP;
MEDILINE-21267165; PubMed-11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                               Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
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Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002006; AAH02006.1; -.
MGD; MGI:1315198; Grcc8.
SEQUENCE 266 AA; 28573 MW; BE0845BA96CF3C57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D74C9AA260DA049C CRC64;
                                                                                01-0CT-2001 (TrEMBLrel. 18, Created)
1-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TY-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MYPU_3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last sequence update)
Last annotation update)
                                  248 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001),
BMBL; AL445564; CAC13498.1; -.
PIR; E90552; E90552.
Mypulist; MYPU 3250; -.
Hypothetical protein; Complete proteome.
SEQUENCE 248 AA; 28555 WW; D74C9AA26
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rich cluster, C8 gene
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Best Local Similarity 100:
Matches 6; Conservative
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                               PRELIMINARY;
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Best Local Similarity
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Blanchard A.;
                                                         Q98QN6;
01-OCT-2001
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Gene

RESULT 3
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10099MAC
099MAC
099MAC
099MMAC
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01-JI
07-JI

088837

RESULT 4 088837 ID 0888: AC 0888: DT 01-N DT 01-N DT 01-N

Matches

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STRAINS of Stella d'Oro; TISSUE=Senescing petals;
MEDLINE=99339248; PubMed=10412903;
MEDLINE=99339248; PubMed=10412903;
Panavas T., Pikula A., Redid P.D., Rubinstein B., Walker E.L.,;
"Identification of senescence-associated genes from daylily petals.";
Plant Mol. Biol. 40:237-248(1999).
HSSP; P24289; 1AKO.
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                            Hemerocallis sp. (Daylily).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales,
Hemerocallidaceae, Hemerocallis.
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Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
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                                                                                        100.0%; Score 25; DB 11; Length 266; 100.0%; Pred. No. 1e+02;
                                                                                                               Indels
                                EMBL; AK010409; BAB26916.1; -.
EMBL. AK028159; BAC35785.1; -.
MMCD; MGL1315198; Grcc8.
SEQUENCE 266 AA; 28708 MW; BE02E77ACAAAC2F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02265; Nuclease; 1.
SEQUENCE 298 AA; 34109 MW; 7FF90F476FFB0057 CRC64;
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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B08K39; C1-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
L-asparaginase II.
ANSA OR PP2453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006309; P:DNA catabolism; IEA.
InterPro; IPR008947; PLC Nuclease.
InterPro; IPR003154; S1/Flnuclease.
                                                                                                              0; Mismatches
                                                                                                                                                                                                               081656 PRELIMINARY, PRT, 081656, 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last seqn 01-OCT-2003 (TrEMBLrel. 25, Last ann
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SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
, AC002397, AAC36014.1; -., AK011313; BAB27539.1; -., AK001606.0; BAB25773.1; -., AK010409; BAB26916.1; -., AK028159; BAC25785.1; -.
                                                                                                                                                                                                                                                                        Senescence-associated protein 6
                                                                              Query Match
Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 6; Conservative
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Q88K39
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EMBL, AL731593; CAD40973.1; --

EMBL, AL731606; CAD41047.1; --
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Foute D.B., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madugu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Utterback R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
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01-0CT-2003 (TYEMBLral. 25, Last sequence update)
01-0CT-2003 (TYEMBLral. 25, Last sequence update)
01-0CT-2003 (TYEMBLral. 25, Last annotation update)
01-0CT-2003 (TYEMBLral. 25, Last annotation update)
05JNBA0027P08.5 procein;
05JNB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Embriton. Microbiol. 4:799-808 (2002).

EMBL; AE016783; AR08065.1; -.

TIGR; PP2453; -.

GO; GO:0006520; P:amino acid metabolism; IEA.

Interpro; IPR006034; Aspidutamnse.

PF00710; Asparaqinase; 1.

PRINTS; PR00139; ASNGINASE.
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PROSITE; PS00191; ASN GLN ASE 2; 1.
Complete proteome.
SEQUENCE 362 AA; 38608 MW; C33F1
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Best Local Similarity 10v...
5 Conservative
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91 ASESIS 96
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Best Local Similarity
Matches 6; Conserv
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|ASESIS 30
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Tikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.",

Nat. Biotechnol. 21:526-531(2003).

EMBL, APOSGO47; BAC74235.1, "Comparative analysis of the industrial language procedure and comparative analysis of the industrial later procedure."

InterProcedure Apparation of the industrial interProcedure and interProcedure. Strategies and interProcedure.

InterProcedure Apparation of the industrial interProcedure. Strategies and in
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonce T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 5; Length 483; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ACOA4759; AAP13762.1;
WormPep; Y37E11AR.7; CE33855.
InterPro; IPR007110; Ig-11ke.
Hypothetical protein.
SEQUENCE 483 AA; 55679 MW; AB174C4F622E3F46 CRC64;
Waterston R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       Waterston R.; Submitted (WAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                  Waterston R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative GTP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 ASESIS 143
                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Bristol N2;
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Q828Y7
   REPRESENTATIONS OF SERVICE SER
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomí,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 25; DB 4; Length 449; Local Similarity 100.0%; Pred. No. 1.9e+02; es 6; Conservative 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
SETAIN-Bristol N2;
Waterston R.H.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL EC047895; AAH47895.1; -.
InterPro; IPR000938; CAP-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Miller N., Maggi L.;
Mithe sequence of C. elegans cosmid Y3/E11AR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 449 449 449 449 AA; 48881 MW; 2C46D1443E143BA8 CRC64;
                        Q86WU4;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
   449 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein Y37E11AR.7. Y37E11AR.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01302; CAP GLY; 2.
PROSITE; PS00845; CAP GLY_1; 2.
PROSITE; PS50245; CAP GLY_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
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SEQUENCE
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Matches
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Membrane GTPase LepA.
LEPA OR PRO0419.
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Best Local Similarity
6; Conserve
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                                                                                                                                                                                                                                                                                            Gaps
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STRAIN-JCSC 4469;
MA X., Ito T., Okuma K., Hiramateu K.;
Ma X., Ito T., Okuma K., Hiramateu K.;
Mistorical distribution of SCCmec allotype in healthcare-associated
MRSA strains in Japan and Prance.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AB097677; BAC76058.1;
Hypothetical protein.
SEQUENCE 543 AA; 62077 MW; 9CD783183EBBF075 CRC64;
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MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical membrane protein.
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  GTP-bindding_dom
                   InterPro; IPR006073; GTP1_OBG.
InterPro; IPR002917; MMR HSR1.
InterPro; IPR002917; MMR HSR1.
InterPro; IPR003255; SMall_GTP.
Pfam, PF01926; MMR HSR1; 1.
PRINTS; PR00326; GTP10BG.
INTERPAMS; TIGR00650; MG442; 2.
TIGREAMS; TIGR00531; small_GTP; 2.
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Best Local Similarity 100.
Matches 6; Conservative
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  InterPro; IPR005289;
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                                                                                                                                                                                                                                                                                                                                                                          319 ASESIS 324
                                                                                                                                                                                       Complete proteome. SEQUENCE 491 AA;
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Q83ZD8;
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STRAIR=SARG / CCMP 1375 / SS120;

MEDLINE=22810154; PubMed=1291746;

Dufresne A., Salanoubat M., Partensky F., Artiquenave F., Axmann I.M.,

Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,

Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,

Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,

Wolf Y.I., Hess W.R.,

"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,

a nearly minimal oxyphototrophic genome.";

Proc. Natl. Acad. SCI. U.S.* 100:10020-10025(2003).
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
NCBI_TaxID=59919;
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MEDLINE=228255999; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
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SEQUENCE 602 AA, 67256 MW, 659E639EBF27D290 CRC64;
EMBL; AL445065; CAC11968.1; --
CO; CO: 0004422; F:metalloendopeptidase activity; IEA.
CO; CO: 0005508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR008915; Peptidase MO;
Pfam; PF02163; Peptidase MSO; 1.
Complete proteome
SCGMPA: 61966 MW; B7829738C56A9B01 CRC64;
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Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
Nature 424:1042-1047(2003).
EMBL: BX575031, CAB18879.1; -.
CCOMplete protecome.
SCOMPLETE FORCE 602 AA; 67457 MW; 5916A6E964658E90 CRC64;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
NCBL_TaxID=74547;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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STRAIN=C57BL/G-0.7 IISSUB=Thymus;
MEDIAINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Ckazaki Y., Muramatsu M., Hayashizaki Y.,
Wonnalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA lbraries for high-rate new gene discovery.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Thymus;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W., Hukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanamori M., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nakamura M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numasaki R., Ohno M., Ohsato N., Okazaki Y., Sarito R., Saitoh H., Sakai K., Sakazume N., Sasaitoh H., Sasaki D., Shibata K., Shhnagawa A., Shiraki T., Sogabe Y., Sanuki H., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20530913; PubMed=11076861; Basaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata Y., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kahliwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Foneda Y., Ishikawa T., Ozawa K., Tanaka T., Ohara E., Watshiki M., Roneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikiki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kanamori M., Suzuki H., Salto R., Muramatsu M., Hayashizaki Y., "T2BP, a Novel TRAP2 Binding Protein, Can Activate NF-kB and AP-1 without TNF Stimulation.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 290:1108-1113(2002).
                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TRAF2 binding protein (TIFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21656991; PubMed=11798190;
   PRELIMINARY;
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                    Q8R011;
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SEQUENCE FROM N.A.
STRAIN=CS/BL/60; TISSUE=Retina;
MEDLINE=CS/BL/60; TISSUE=Retina;
MEDLINE=25/BL/60; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
HARALYSIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Xu C.S., Li W.Q., Li Y.C., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
"Liver regeneration after PH.";
"Liver regeneration after PH.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX925204; AAP92605.1;
ERBL, AX355204; A4878 MW; 732807ADD8AE3D4D CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 11; Length 421; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                    EMBL; AKO41891; BAB86846.1; -.
EMBL; ABO6211; BAB86903.1; -.
EMBL; ABO6211; BAB86903.1; -.
EMBL; ABO6211; BAB86903.1; -.
MJD; MJ:218265; T2bp.
GO; GO:0007249; PINK-Ir-kappaB/NF-kappaB cascade; IDA.
GO; GO:0007249; PINK-Ir-kappaB/NF-kappaB cascade; IDA.
InterPro; IPR008984; SMAD_FHA.
SMRAT; SM02240; FHA.
PROSITE; PSSGO066; FHA.
PROSITE; PSSGO066; FHA.
SRQUENCE 184 AA; 21560 MW; 1466F2A7307F03B2 CRC64;
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"TIFA, a novel TRAF6 binding protein.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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D QTP45
AC QTP45;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 QENNWPT 156
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Matches 6; Conserv
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Best Local Similarity
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Query Match
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0
                                                                                                                                  SEQUENCE FROM N.A.

CENTAIN=ATC 19989 / CB15;

MEDLINE=21173698; PubMed=11259647;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

A Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A POTOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Colonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Utcerbeck T., Tran K., Wolf A., Vamathevan J., Ermelaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R PIR; AB0321; A87321.

R TIGR; CCO579; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAID=CO-92 / Biovar Orientalis;
STRAID=CO-92 / Biovar Orientalis;
STRAID=CO-92 / Biovar Orientalis;
BrEDINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W. Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamilin N., Hollroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Versinia pestis.
Batezria: Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriacae, Yersinia.
VCBI_TaxID=632;
                                             Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 40; DB 16; Length 972; 75.0%; Pred. No. 1.9e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       972 AA; 104732 MW; B599CDD10C26AC4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative membrane protein (Putative sulfatase)
YPO1260 OR Y2924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1007 GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006815; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR00531; TonB boxC.
Pfam; PF00593; TonB dep_Rec; I.
Receptor; Complete protecme.
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Matches 6; Conservative
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                         Caulobacter crescentus.
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                                                                                       NCBI_TaxID=155892;
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MEDLINE=20196006; PubMed=10731132,

MEDLINE=20196006; PubMed=10731132,

Adams M.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wordman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Abril J.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Abrons R., Doup L.E., Downes M., Digarn-Rocha S., Dunkov B.C., Dunn P.,

Dodson K., Doup L.E., Downes M., Digarn-Rocha S., Dunkov B.C., Dunn P.,

Bookson K., Doup L.E., Downes M., Digarn-Rocha S., Planck J.,

Abraris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Alalai M., Kalush F., Karpen G.H., Re. Z., Kennison J.A., Ketchum K.A.,

Lasko P., Lei Y., Mattel B., McIntosh T.C., McLeod M.P., Moshersin D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puris V., Resee M.G.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puris V., Resee M.G.,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endotterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                              R PIR; ACULASTA; ACCOUNTS.

R GO; GO: 0016020; C: membrane; IEA.

GO; GO: 0008481; F: receptor activity; IEA.

R GO; GO: 0008481; F: resultinic ester hydrolase activity; IEA.

R GO; GO: 0008515; F: resultinic ester hydrolase activity; IEA.

R GO; GO: 0008152; F: resultinic ester hydrolase activity; IEA.

R GO; GO: 0008152; F: resultinic ester hydrolase activity; IEA.

R GO; GO: 0008152; F: resultinic ester hydrolase activity; IEA.

R GO; GO: 0008152; F: resultinic ester hydrolase activity; IEA.

R GO; GO: 0008152; F: resultinic ester hydrolase activity; IEA.

R InterPro; IPR000815; Sulfatase.

R Ffam; PF00884; SUlfatase; I.

R PR03ITE; PS00430; TONB DEPENDENT REC 1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 16; Length 598;
Pred. No. 2.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein; Complete proteome.
598 AA; 67474 MW; C6EE2A0BDC1E43A2 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CG7958 protein (LD16921p).
"Genome sequence of Yersinia pestis KIM.";
Dacterio1. 184:6601-4611(2002).
EMBL; AJ414147; CAC90094.1; -.
EMBL; AE013894; AAM86475.1; -.
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1es 6; Conservative
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SEQUENCE 59
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RESULT 7

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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J. W., Center A., Champe M., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirekas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spiue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spiadling A.C., Stapleton M., Strong R., Sun B., Svirskas R., Tedtor C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhang M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhou M., Zhou X., Zhu S., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Spith H.O. Science 287:2185-2195(2000).
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Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Mistra S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D.,
Tradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Rarris N.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
"Annotation of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=y; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 4.7e+02;
0; Mismatches 3; Indels
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EMBL; AE003547; AAF50134.2; -.
EMBL; BT003272; AAO25029.1; -.
FlyBase; FBgn0036103; tna.
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InterPro; IPR004181; Znf MIZ.
Pfam; PF02891; zf-MIZ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%;
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Best Local Similarity 66.,
6, Conservative
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Lin Q., Zhi N., Ohashi N., Horowitz H.W., Aguero-Rosenfeld M.E.,
Lin Q., Zhi N., Ohashi N., Horowitz R. Rikihisa Y.,
Raffalli J., Wormer G.P., Rikihisa Y.,
"Analysis of Sequences and Loci of p44 Homologs Expressed by Anaplasma phagocytophila in Acutely Infected Patients.";
Clin. Microbiol. 40:2981-2988 (2002).
EMBL, Ayods19; AAL78182.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                Afonco C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L., Rutish G.F., Rock D.L.;

Rutish G.F., Rock D.L.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF410153; AAL69787.1; -.

GO; GO:0016020; C:membrane; I.E.

GO; GO:0007156; P:homophilic cell adhesion; IEA.

InterPro; IPR002156; Cadherin.

Hypothetical protein.

SEQUENCE 111 AA; 13043 MW; AF715FFF23E704EB CRC64;
                                                                                                                                                                                                        STRAIN=17077-99;
MEDLINE=21624277; PubMed=11752168;
AGDING C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Sock D.L.;
"The genome of swinepox virus.";
J. Virol. 76:783-790(2002).
                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 12; Length 111;
Pred. No. 66;
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                          Q8V3P6;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
SPV049 hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
44 kDa major outer membrane protein (Fragment).
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Pred. No. 77;
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            111 AA
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87.5%;
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71.4%;
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NCBI_TaxID=948;
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Best Local Similarity 87....
7; Conservative
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              PRELIMINARY;
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                                                                                                                  Swinepox virus.
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SEQUENCE FROM N.A.

STRAIN=EL TOT N16961 / Serotype 01;

MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

MEDGEG V.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

McDonald L., Uwmathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
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IJdo J W., Wu C., Telford S.R., Pikrig E.;
"Differential expression of the p44 gene family in the agent of human
granulocytic ehrlichiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Anaplasma.
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Pred. No. 91;
2; Mismatches 1; Indels
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF512671; AAP14021.1; -.
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TIGR: VC1803; .
Hypothetical protein; Complete proteome
SEQUENCE 153 AA; 17480 MW; C92B7B307501A722 CRC64;
                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VC1803.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence updat
01-JUN-2003 (TrEMBLrel. 24, Last annotation upo
Major outer membrane protein SC1-1.(Fragment).
                                                                                                                                                                                                                                                                      153 A.A.
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EMBL; AE004257; AAF94952.1; -.
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89 NHWWPTS 95
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Infect. Immun. 71:1706-718 (2003).
EMBL, AX164497; AA030109.1; -.
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Infect. Immun. 71:1706-718 (2003).
EMBL. AX164505; AAO30117.1; -.
      Gaps
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Lundgren A.M., Alleman A.R., Wong S.J., Chu F.K., Munderloh U.G.,
Jauron S.D.;
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BELLINE-25541496; PubMed=12654783;

Barbet A.F., Meeus P.F.M., Belanger M., Bowie M.V., Yi J.,

Lundgren A.M., Alleman A.R., Wong S.J., Chu F.K., Munderloh U.G.,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Major surface protein 2 (Fragment)
Anaplasma phagocytophilum (Ehrlichia phagocytophila),
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
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   Indels
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14576 MW; 6C96C03CC55E121A CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Major surface protein 2 (Fragment)
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STRAIN=var B;
MEDLINE=22541496; PubMed=12654783;
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NCBI_TaxID=948;
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NCBI_TaxID=948;
Conservative
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139 AA;
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Best Local Similarity
Matches 5; Conserv
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"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Mucleic Acids Res. 30:5293-5300(2002).
EMBL, AP004170; BAC43791.1;
                                                                                                                                                                                                                                                                                                                        STRAIN=HZ;
MEDLINB=21843103; PubMed=11854198;
MEDLINB=21843103; PubMed=11854198;
Zhi N., Ohashi N., Tajima T., Mott J., Stich R.W., Grover D.,
Telford S.R. III, inn Q., Rikthisa Y.;
"Transcript heterogeneity of the p44 multigene family in a human granulocytic christiniosis agent transmitted by ticks.";
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                                                                                                                                                                                                                                                 Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Anaplasma.
NCBI_TaxID=948;
                                           Query Match 66.1%; Score 37; DB 2; Length 166; Best Local Similarity 71.4%; Pred. No. 99; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 178;
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            166 166
166 AA; 17205 MW; 6997EFAD6D745C34 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chromcomal replication initiator protein.
MYPE10.
                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major outer membrane protein P44-16 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.1%; Score 37; DB 2; I 71.4%; Pred. No. 1.1e+02; ative 1; Mismatches 1;
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Best Local Similarity 71.4
Matches 5; Conservative
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005689; F:DNA replication origin binding; IEA.
GO; GO:00066; F:DNA replication origin binding; IEA.
GO; GO:000677; P:Nucleotide binding; IEA.
GO; GO:0006275; P:regulation of DNA replication; IEA.
InterPro; IPRO0359; Para ATPase.
InterPro; IPRO0359; Para DnaA.
Pfam; PF00308; bac dnaA; 1.
PRINTS; PR00051; DNAA.
PRINTS; RR0052; DNAA; 1.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE011207; AAN47355.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 503 AA; 57820 MW; C50EFFADC2366792 CRC64;
                                                                                                                                                                                                                                                                                                                             452 AA; 52977 MW; A853FC934F25F0E2 CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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85.7%; Pred. No. 3.1e+02;
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280 NNNYPTT 286
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AMEDINE=77038198; PubMed=824717;
A Capra J.D., Klapper D.G.; Capra J.D., Klapper D.G.;
Capra J.D., Klapper D.G.; Capra J.D., Klapper D.G.;
Capra J.D., Klapper D.G.; Capra J.D., Klapper D.G.;
Capra L.G. Capra J.D., Klapper D.G.;
Capra L.G. Capra J.D. Capra J.C. Cap
              Q12659 penedeuc
P09849 orycrolagus
P09849 orycrolagus
O23676 arabidopsis
Q9m2K6 macaca mula
P24017 klebaiella
P21613 drosophila
P20034 escherichia
P2735 serraria ma
P34941 arbacia lix
O51402 borrelia bu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLENTARITY-DETERMINING-3.
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BY SIMILARITY.
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11834 MW; 739993A95431434A CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; Immunoglobulin V region.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) cellulose-growth-specific protein precursor.
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                                                    GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobuliv region; Signal.
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Klapper D.G., Capra J.D.;
From amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Paris) 1272:s61-271(1976).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACITVITY.
PIR; A01897; K3HUPM.
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDNed=3083417; MEDLINE=86177570; PubNed=3083417; Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Goldfien R., Carson D.A.; Caloning and sequence determination of a human rheumatoid factor
                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region CLL precursor (Rheumatoid factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 42; DB 1; Length 109; 77.8%; Pred. No. 1.7; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                 21-JUL-1986 (Rel. 01, Created)
21-ULL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g kappa chain V-III region POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA
                                          109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P80362, IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
INTERFO; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00047; ig; 1.
SMAART, SMO4066; IGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 OYNWWPPT 98
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                                                                                                                                                                         Homo sapiens (Human).
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P04207;
                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                             KV3F HI
P01624
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Armesilla A.L., Thurston C.F., Yaguee E.;
Armesilla A.L., Thurston C.F., Yaguee E.;
Armesilla A.L., Thurston C.F., Yaguee E.;
bisporus during growth on crystalline cellulose.";
FEMS Microbiol. Lett. 116:293-299(1994).
-:- FUNCTION: PROBABLE GLYCOSYL HYDROLASE ACTIVE ON CELLULOSE..
-:- SUBCELLULAR LOCATION: Secreted..
-:- SUBCELLULAR: CONTAINS: Fungal-type cellulose-binding (CBD) domain..
-:- SIMILARITY: Contains I fungal-type cellulose-binding (CBD) domain..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=93012985; PubMed=1398098;
MEDLINE=93012985; PubMed=0.A., Thurston C.F.;
"Isolation and characterization of a cellulose-growth-specific gene from Agaricus bisporus.";
Gene 119:183-190(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agaricus bisporus (Common mushroom).
Eukaryota, Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
IG KAPPA CHAIN V-III REGION CLL. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-3.
JKI SEGMENT.
BY SIMILARITY.
                                                                                                                                             COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 129;
Pred. No. 9.1;
0; Mismatches 1; Indels
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SEQUENCE
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    SOUR DEPARTMENT OF THE PROPERTY OF THE PROPERT
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Denizot F., Devine K.M., Dusterbhóff A., Brhiloh S.D., Emmerson P.T.,
Entian K.D., Errington J., Pabret C., Ferrari E., Foulger D., A
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                  HSSP, P00725; 2CBH.
InterPro; IPR000254; CBD fungal.
InterPro; IPR000334; CBD fungal.
InterPro; IPR00333; GlyCo_hydro_61.
Pfam; PF00443; GlyCo_hydro_61; 1.
Pfam; PF04443; GlyCo_hydro_61; 1.
SMART; SM00236; fCBD; 1.
Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EC 5.3.1.17)
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MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                              CELLULOSE-GROWTH-SPECIFIC PROTEIN.
                                                                                                                                                                                                                                                                                                             CATALYTIC (POTENTIAL).
LINKER (POTENTIAL).
CELJULOSE-BINDING (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60E2C8080895CA2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
4-deoxy-t-threo-5-hexosulose-uromate ketol-isomerase keto-4-deoxyuronate isomerase) (DKI isomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB Pred. No. 23;
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    33754 MW;
                                                            EMBL; M86356; AAA53434.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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162 QNNSWTTT 169
                                                                                  JC1311; JC1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QNNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                     303
163
320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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P50843;
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
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CARBOHYD
SEQUENCE
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KDUI_BACSU
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Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Rad Parro V., Pohl T.M., Portetalle D., Porwollik S., Prescott A.M.,
Resecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Reger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
Rato T., Scanlan E., Schleich S., Schroeter R., Socifone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tamakoshi A., Tahaka T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Tarahashi H., Takemaru K.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
Subtilis ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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SEQUENCE FROM N.A.
MEDLINE=89345533; PubMed=2668944;
Yamawaki-Kataoka Y., Tamaoki T., Choe H.-R., Tanaka H., Kataoka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: 4-deoxy-L-threo-5-hexosulose uronate = 3-deoxy-D-glycero-2,5-hexodiulosonate.
-!- PATHWAY: Pectin degradation.
-!- SIMILARITY: Belongs to the kdul family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isomerase; Complete proteome.
SEQUENCE 275 AA; 31135 MW; 31B2CE2CE7C54760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1;
Pred. No. 29;
0; Mismatches
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EMBL; Z99115; CAB14130.1; -.
PIR; E69648; E69648;
Subtilist; BG11401; kduI.
HAMAP; MF 00687; -; 1.
InterPro; TPR007045; KduI.
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 QNNNWNT 189
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QNNNWPT 8
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P14605;
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The Schiedarschandovers pombe and Saccharomyces correvisiae.",

Res SUNDANCE PROVE N. A.

RES SUNDANCE FOR N. A.

RES SUNDANCE PROVE N. B.

RES SUNDANCE R.

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      PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50200; RA; 1.
Lyase; Repeat; Leucine-rich repeat; cAMP biosynthesis; Metal-binding; Magnesium.
292 380 RAS-ASSOCIATING.
REPEAT 385 403 LRR 1.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=81220975; PubMed=6264318;
Pech M., Hochtl J., Schnell H., Zachau H.G.;
"Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:668-670(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                        Length 1692;
                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 169
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
W; D137CBE8770A8655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TV51_MOUSE STANDARD, PRT; 115 AA.
P01642;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig kappa chain V-V region L7 precursor (Fragment).
                                              RAS-ASSOCIATING.

LRR 1.

LRR 2.

LRR 3.

LRR 4.

LRR 5.

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LRR 9.

LRR 9.

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LRR 11.
                                                                                                                                                                                                                                                                                                                     1692 AA; 190333 MW;
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PDB; 1J10; 18-FEB-03.
PDB; 1J17; 18-FEB-03.
INTERPRO; 1B-FEB-03.
INTERPRO; 1PR00310; 1g-like.
INTERPRO; 1PR003596; Ig_v.
Ffam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                        66.1%;
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nes 5; Conservative
SM00314; RA; 1
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INKED (GLCNAC. ..) (POTENTIAL)
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Pred. No.
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MEDLINE-21481446; PubMed=11597768;
Nakajama D., Nakajama M., Kikuno R., Hirosawa M., Nagase T., Ohara O.
Nakajama D., Nakajamama M., Kikuno R., Hirosawa M., Nagase T., Ohara O.
"Identification of three novel non-classical cadherin genes through
comprehensive analysis of large cDNAs.";
Brain Res. Mol. Brain Res. 94:85-95(2001).
-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells. Cadherin 23 may function as hair
bundle organizer perhaps by cross-linking the stereocilia (By
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                           IG KAPPA CHAIN V-V REGION L7.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                  FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                   64.3%; Score 36; DB 1; Length 115; larity 71.4%; Pred. No. 17; Conservative 2; Mismatches 0; Indels
                                                                                                                                                           C17BEC758C577E00 CRC64;
 Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
CDH23 DR KIPAN1774.
                                                                                                                               BY SIMILARITY.
                                                                                                                                                            12615 MW;
   V region;
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115 AA;
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5; Conserv
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Immunoglobulin
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson S.M., Householder D.B., Coppola V., Tessarollo L., Fritzsch B., Lee E.-C., Goss D., Carlson G.A., Copeland N.G., Jenkins N.A.; "Mutations in Cdh23 cause nonsyndromic hearing loss in waltzer mice."; Genomics 74:228-233 (2001).
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Di Falma P., Holme R.H., Bryda B.C., Belyantseva I.A., Pellegrino R., Kachar B., Steel K.P., Noben-Trauth K., "Mutations in Calals, encoding new type of cadherin, cause stereocilla disorganization in waltzer, the mouse model for Usher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [5]
GENOMIC ORGANIZATION, ALTERNATIVE SPLICING, VARIANT WALZER
2718-ASN-GLU-PRO-2720 DEL, AND VARIANTS PRO-5; VAL-229; LYS-891;
ILE-1137; ARG-1236; VAL-2025; VAL-2026; THR-2217; HIS-2222; ARG-2270
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation of a full-length mouse cDNA collection.";
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  Indels
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Fu Y., Wang Q., Roe B.A.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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MEDLINE=11623040; PubMed=11750125;
Di Palma F., Pellegrino R., Noben-Trauth K.;
  Mismatches
                                                                                                                                                                                                                                                                        (Otocadherin)
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=20578758; PubMed=11138008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21280917; PubMed=11386759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                     099PF4; 099MH1; 09D4M9; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seqn 10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syndrome type 1D.";
Nat. Genet. 27:103-107(2001).
  5; Conservative
                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                      Cadherin-23 precursor
                                                                       2061 NDNWPT 2066
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                    3 NNNWPT 8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                Isozdagogppr4-2; Sequence-VSP_000648;
Isosub SPECIFICITY: In adult animals relatively high levels of expression are found in testis, skeletal muscle, heart, eye and thymus, and lower expression in kidney, lung and brain. Found in the sensory hair cells of the inner ear.

ISDEAASE Defects in CDH23 are the cause of Maltzer (v) phenotype. Waltzer mice are characterized by deafness and vestibular dysfunction due to degeneration of the neuroepithelium within the
"Genomic structure, alternative splice forms and normal and mutant alleles of cadherin 23 (Gdh23).";
Gene 281:31-41(2001).
-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells. Cadherin 23 may function as hair bundle organizer perhaps by cross-linking the stereocilia.
-!- SUBCELULAR LOCATION: Type I membrane protein (By similarity).
-!- ALTERNATIVE PRODUCTS:
EVent-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal; Multigene family; Alternative splicing; Deafness; Polymorphism; Disease mutation.
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EXTRACELLULAR (POTENTIAL)
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CADHERIN 1.
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CADHERIN 17.
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EMBL; AVG5662; AAK07670.1; -.
EMBL; AXC016365; -; NOT_ANNOTATED_CDS.
EMBL; AC079818; -; NOT_ANNOTATED_CDS.
EMBL; AC079818; -; NOT_ANNOTATED_CDS.
EMBL; AC079819; -; NOT_ANNOTATED_CDS.
HASP; P15.116; 1NGJ.
MGD; MGI.1890219; CAND.
GO; GO:000529; C:cilium; IDA.
GO; GO:000529; C:cilium; IDA.
GO; GO:0005529; C:cilium; IDA.
InterPro; IPR002126; Cadherin.
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PROSITE; PS00232; CADHERIN 1; 17.
PROSITE; PS50268; CADHERIN 2; 27.
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PRINTS; PR00205; CADHERIN.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=S2886 / AB972;

MEDIINE=97313267; FubMed=9169871;

MEDIINE=97313267; FubMed=9169871;

A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Flocht M., Goffeau A., Hebling U., Heumann K., A., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moetter P., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portecelle D., Purnealle B., Rechmann S., Rieger M., Rinke M., Rinke M., Scherens B., Scholler P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; II."; Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION.
MEDLINE-21468387; PubMed=11583615;
Bassler J., Grandi V., Gadal O., Lessmann T., Petfalski E.,
Tollervey D., Lechner J., Hurt E.;
"Identification of a 608 preribosomal particle that is closely linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to nuclear export.", Mol. Cell 8:517-52(2011).
-i- FUNCTION: May function as a nuclear chaperone and be involved in the assembly/disassembly of macromolecular complexes in the
                                                                                 28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Midasin (MIDAS-containing protein).
MDN1 OR YLR106C OR L8004.13.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceses; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
PubMed=12102729;
Garbarino J.E., Gibbons I.R.;
"Expression and genomic analysis of midasin, a novel and highly conserved AAA protein distantly related to dynein.";
BMC Genomics 3:18-18(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleus.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 VMFA domain.
                                              STANDARD;
                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                          MDN1 YEAST
Q12019;
    RESULT 10
MDN1_YEAST
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Pred. No. 5.4e+02;
1; Mismatches 0; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984).
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                                                                                                                                                                                                                                                                                    64.3%; Score 36; DB 1; Length 4910;
100.0%; Pred. No. 8e+02;
Live 0; Mismatches 0; Indels
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COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                                                                                                                                                                            4910 AA; 559302 MW; E4E873BEDF6E1E5B CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region VG precursor (Fragment).
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
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PIR; A01900; K3HUVG.
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MRARI, SM00406, IGV; 1.
PROSITE, PS50835, IG LIKE; 1.
Immunoglobulin V region; Signal.
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SHRAINE-20365717; PubMed=10910347;

SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

ALVarenga R., Alves L.M.C., Araya J.E., Baia G.S., Bapista C.S.,

Barros M.H., Bonacocraf E.D., Bordin S., Bove J.M., Briones M.R.S.,

Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

Colauto C.Olombo C., Costa M.C.R., Costa P.F., Costa M.C.R., Costa-Neco C.M.,

A Farga J.S., Franca S.C., Franco M.C., Fronme M., Furlan L.R.,

A Garnicani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

A Garnicani M.P., Junqueira M.H.S., Gomes S.L., Gruber A.,

A Garnicani M.H., Junqueira M.H.S., Gomes S.L., Gruber A.,

A Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

A Garnicani M.P., Mardine E.E., Lambais M.R., Leite L.C.C.,

A Marques M.V., Martins E.A., Martins E.M.F., Martino C.L.,

A Mardine B.A., Nascimento A.L.T.O., Netto L.E.S.,

Monn D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

A de Oliveira M.C. de Oliveira R.C., Pereira H.A. Jr., Perguero J.B.,

A Gasilva A.C., da Silva A.M., da Silva F.R., Silva M.A. Jr.,

A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A., Jr.,

A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A., Tsuhako M.H.,

A da Silva A.C.R., Santelli R.V., Sawasaki H.E.,

A Goldwan M.P., Turffil D., Tsai S.M., Tsuhako M.H.,

A Goldwan M.P., Zatz M., Mardinis J., Setubal J., Cettore A.L.,

A Goldwan M.P., Zatz M., Werjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Zatz M., Werjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Verjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Verjovski-Almeida S., Vettore A.L.,

A Goldwan M. Sulva M.A., Verjovski-Almeida S., Vettore A.L.,

A Goldwan M. Sulva M.A., Verjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Zatz M., Werjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Zatz M., Werjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Zatz M., Werjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Salva M.A., Verjovski-Almeida S., Vettore A.L.,

A Goldwan M.P., Martin S. M. Salva
                                                  Gaps
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Nature 406:151-159(2000).
-!- FUNCTION: Involved in DNA repair (By similarity).
-!- SIMILARITY: Belongs to the radc family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                               ..
  1; Length 115;
                                               1; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Score 35; DB
Pred. No. 25;
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PROSITE; PS01302; RADC; 1.
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Interpro; IPR001405; RadC.
Pfam; PF04002; RadC; 1.
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Query Match 62.5
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                       RADC XYLFA
Q9PGZ8;
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RADC_XYLFT RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-KI2;

MEDLINE-97349980; PubMed=9205837;

MEDLINE-97349980; PubMed=9205837;

MEDLINE-97349980; PubMed=9205837;

MA toh T., Kimura S., Kitagawa M., Makino K., Miki T., Miteuhashi N.,

Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

Magada S., Horiuchi T.,

Managata S.,

Managata S.,

Managata S.,

Managata S.,

Managata Managat
                                                                                                                                                                                                                                                                                                                                                                                                                        Gowrishankar J.; "Nucleotide sequence of the osmoregulatory proU operon of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIZ / MG1655,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycine betains/L-proline transport system permease protein prow.
PROW OR B2678.
Escherichia coli.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000352; AAC757255.1; -.
EMBL; AE000352; AAC757255.1; -.
EMBL; D90691; BAA16543.1; -.
EIR, J50129; MMECPH.
Eccdene; BG10772; proW.
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BD_transp; 1.
PROSITE; PS50928; AEC TMI; 1.
Transport; Amino-acid_transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL) POTENTIAL.
                             354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli.";
J. Bacteriol. 171:1923-1931(1989).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gowrishankar J.;
J. Bacteriol. 172:1165-1165(1990).
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89197759; PubMed=2649479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M24856; AAA24428.1; -.
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DOMAIN 1
TRANSMEM 100
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                             ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERRATUM
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MEDINE=22421331; PubMed=12533478;

MADANIC CY. Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

MAYAKI C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Marino C.L., Giglioti E., Abreu I.L., Romavan F.S., Celestino A.V.,

Ad Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

A Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,

Kitajima J.P.,

"Comparative analyses of the complete genome sequences of Pierce's

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dissesse analyses of the complete genome sequences of Pierce's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA repair procein rado homolog.
RADC OR PD0117.
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales;
                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                     62.5%; Score 35; DB 1; Length 224; 100.0%; Pred. No. 50;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, MF 2010; -; 1.
InterPro; IPR001405; RadC.
Pfam; PF04002; RadC; 1.
PROSITE; PS01302; RADC; 1.
PROSITE; PS01302; RADC; 1.
SEQUENCE 224 AA; 24590 MW; E84351E63C8AF775 CRC64;
  224 AA; 24618 MW; 474351E63C880A5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fastidiosa.",
J. Bacteriol. 185:1018-1026(2003).
--!- FUNCTION: Involved in DNA repair (By similarity).
-!- SIMILARITY: Belongs to the radC family.
                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last seguence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      224 AA.
                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE012553; AA028016.1; -.
                       Query Match
Best Local Similarity 100...
5, Conservative
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Best Local Similarity luv...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=183190;
                                                                                                                                                                 4 NNWPT 8
                                                                                                                                                                                               4 NWWPT 8
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                                                                                                                                                                                                                                                                                                                                                                RADC XYLFT
Q87F21;
SEQUENCE
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RESULT 14

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Thu Oct 14 09:36:54 2004

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MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan
to a new 4-position in an acceptor, which may be glucose or (1,4).
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-D-glucan.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the disproportionating enzyme family.
                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE001283; AAC67678.1; --
PIR, G71557, G71557.
PIR, G71557, G71557.
PIR, BR003385; Glyco_hydro_77.
PERM; PF02446; 4A, Glucanotrans; I.
TIGRFAMS; TIGR002I7; malQ; 1.
Transferases; Glycosyltransferase; Carbohydrate metabolism; Complete proteon.cs 527 AA; 61453 MW; 52455D5E9ED2046D CRC64;
                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1; Length 354;
Pred. No. 79;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.5%; Score 35; DB 1; Length 527; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
(Disproportionating enzyme) (D-enzyme).
                                                     CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL),
D35F94A74E2779D1 CRC64;
                                                                                                                                                                                                                       PERIPLASMIC (POTENTIAL).
  PERIPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                             37619 MW;
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75.0%;
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Matches 6; Conservative
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1171
1219
2219
2270
2291
3300
351
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                                                                                                                                                                                                                                                                                                                354 AA;
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SEQUENCE FROM N.A.
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ALO CHITR

AC 084089;
DT 30-MAY-2000
DT 30-MAY-2000
DT 16-OCT-2001
DE 4-alpha-gluca
DE 4-alpha-gluca
DE 4-alpha-gluca
DE ACT-2001
DE 16-OCT-2001
DE 16-OCT-2001
DE 16-OCT-2001
DE CALLANDIA
DE 10-OCT-2001
RN III
RN III
RN III
RN III
RN SEQUENCE FRO
RX MEDINES-9900
RX MEDINES-9900
RX MEDINES-9900
RX MICCHOLL W.P.
RX MICCHOLL W.P.
RX MICCHOLL W.P.
CC -1-CALLANDIA
CC -1-CALLANDIA
CC -1-SIMILARI
CC -1-S
DOMAIN
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Db 186 NHWPTT 191
Search completed: October 6, 2004, 16:30:32
Job time : 7.55632 secs
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; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-36
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Sequence 112, Appl
Sequence 112, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 20, Appl
Sequence 21, Appl
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                                                                                                    October 6, 2004, 16:34:15 ; Search time 56.0526 Seconds (without alignments) 51.669 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: Ggn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.ppp:*
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11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.ppp:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-996-954B-12
US-10-374-600-112
US-10-374-600-112
US-10-374-600-114
US-10-374-600-20
US-10-374-600-22
US-10-374-600-23
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US-10-374-600-23
US-10-374-600-23
US-10-374-600-23
US-10-374-600-5
US-10-374-600-5
US-10-374-600-1
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                                                                                                                                                                                                                                                                                                         1351062 segs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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56
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Maximum DB seq length: 200000000
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Perfect score:
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US-10-374-600-17 US-10-374-511-5 US-10-374-531-11 US-10-374-531-15 US-10-374-531-11 US-10-374-531-11 US-10-374-531-11 US-10-374-531-17 US-10-374-531-17 US-10-374-531-17 US-10-453-698-13 US-10-453-698-130 US-10-453-698-130 US-10-453-698-130 US-10-453-698-132 US-10-313-132 US-10-313-133-133-133-133-133-133-133-133-
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## ALIGNMENTS

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US-90-798-809-36

DUS-198-98-98-36

Publication No. US20030103973A1

GENERAL INFORMATION:

APPLICANT: ROCKWell, Particia

APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE SPERENCE: Sequence Listings 1-41 for 381-25 CIP

TITLE OF INVENTION: Member: US/09/798,689

FILE REPERENCE: Sequence Listings 1-41 for 381-25 CIP

CURRENT PELING DATE: 2001-03-02

FRIOR APPLICATION NUMBER: 08/967,113

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-3

PRIOR FILING DATE: 1996-09-03

PRIOR FILING DATE: 1996-09-03

PRIOR FILING DATE: 1996-09-03

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20
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100.0%; Score 56; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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1 QONNNWPTT 9

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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
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                                                                                                US-09-996-954B-12

Sequence 12. Application US/09996954B

Publication No. US20030157104A1

GENERAL INFORMATION:

APPLICANT MAKSAI. HATIAN W.

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

CURRENT APPLICATION NUMBER: US/09/996,954B

PRIOR FILING DATE: 02-124-2001

PRIOR PILING DATE: 04-124-2001

PRIOR APPLICATION NUMBER: 09/314,028

PRIOR APPLICATION NUMBER: 09/312,284

PRIOR FILING DATE: 05-14-1999

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
ITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 56; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/08/973,065C
RILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
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APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens-Rodent Chimera
US-09-996-9548-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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DONNNWPTT
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US-10-374-600-112
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Gaps
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TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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MEDIUM TYPE: Diskette 3,5 inch 1,44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COURTER: IBM compatible
CORRENT SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: BCT/US96/09847
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/82,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/82,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
  11245/46003
                                                                                                                                            ; TYPE: amino acids
; TYPE: amino acids
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-374-600-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-10-374-531-112
Sequence 112, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                       425-5288
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                                                               TELEFAX: (212) 425-52
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 112 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
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US-10-374-531-114
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Publication No. US20030224001A1
GENERAL INFORMATION:
GENERAL INCLORE Systems Incorporated, et al.
APPLICANT: Inclore Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 56; DB 12; Length 107; larity 100.0%; Pred. No. 0.18; Conservative 0; Mismatches 0; Indels
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CUDUNIATIONS
CUDUNIATIONS
CIDENTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: Diskette 3.5 inch 1.44 Mb storage
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION AUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INPORMATION:
NUMBER/AGENT INPO
                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                Query Match
100.0%; Score 56; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
MOLECULE TYPE: peptide HYPOTHERICAL: NO PREACMENT TYPE: internal PREQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX: (212) 425-5288
SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Ke
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                      1 QONNNWPTT
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                      US-10-374-531-112
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                                                                                                                                  Sequence 114, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; TIPLE OF INCLONE Systems Incorporated, et al.
ITLE OF INVENTION: ANTIBODY AND ANTIBODY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Ms-Dos
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 10-Mar-1996
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: Deborah & Somerville
REGISTRATION NUMBER: 31,995
TELECOMMUNICATION NUMBER: 31,995
TELECOMMUNICATION NUMBER: 31,995
TELECOMMUNICATION NUMBER: 31,995
TELECOMMUNICATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHERICAL: NO FRAGWENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
TOPOLOGY: not relevant
ULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York COUNTRY: US
89 QQNINWPTT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 QONNNNPTT 97
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US-10-374-600-20
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Gaps

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Indels

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar 1998
APPLICATION NUMBER: PCT/USS6/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
RAME: DEDOCRAP A. SOME-Y111E
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECHONER: (212) 425-7200
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FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
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APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                            APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-10-374-600-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDMESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                           SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-374-600-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: IMClone Systems Incorporated, et al.
TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-MAT-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCEDOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | LENGTH: 113 amino acids | FYER: amino acids | FYER: amino acids | FYER: amino acid | FAEGMENT TYPE: peptide | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-10-374-600-20
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Peb-2003
CLASSIFICATION: <UNKNOWN>
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CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                    ADDRESSEE: Kenyon & Kenyon STREET: One Broadway CITY: New York STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                     NUMBER OF SEQUENCES: 120
                                                 CORRESPONDENCE ADDRESS:
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
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Gaps
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100.0%; Score 56; DB 15; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
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APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: VUNBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
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REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPRAK: (212) 425-5288
                                                                                                               LENGTH: 113 amino acids
TYPE: amino acid
STANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECTLE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon STRET: One Broadway CITY: One York STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                   425-5288
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           TELEFAX: (212) 425-5:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 120
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US-10-374-531-22
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100.0%; Score 56; DB 12; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 20, Application US/20040006212A1
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible COMPUTER: IBM compatible COMPUTER: IBM compatible COMPUTER: IBM compatible CORPERATION SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION NUMBER: US/10/374,531

FILING DATE: 25-Feb-2003

CLASSIFICATION NUMBER: US/08/973,065C

FILING DATE: 19-Mar-1998

APPLICATION NUMBER: US 08/482,982

FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/482,982

FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/482,982

FILING DATE: 10-MC-1995

APPLICATION NUMBER: US 08/573,289
FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/573,289

FILING DATE: 15-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Deborah A. Somerville

REGISTRATION NUMBER: 31,995

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | JENGTH: 113 amino acids | JENGTH: 114 amino acids | JENGTH: 115 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 425-5288 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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COUNTRY: US
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TELEFAX: (212) 425-E
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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                 JS-10-374-600-5
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US-10-374-531-23
is Sequence 23, Application US/10374531
js Publication No. US20040006212A1
js Publication No. US20040006212A1
js GENERAL INFORMATION:
js APPLICANT: InClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR TITLE OF INVENTION: 120
                                     100.0%; Score 56; DB 15; Length 113; 100.0%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 56; DB 15; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOPERATING SYSTEM: MS-DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/ABONT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | LENGTH: 113 amino acids | LENGTH: 113 amino acids | TYPE: amino acids | TYPE: amino acids | STRANDEDNESS: not relevant | MOLECULE TYPE: peptide | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-10-374-531-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
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                                                                              9; Conservative
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                                                                                                                        1 QONNNWPIT 9
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                                     Query Match
Best Local Similarity
Matches 9; Conserv
US-10-374-531-22
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Sequence 11, Application US/10374600

Sequence 11, Application US/10374600

Publication No. US2003224001A1

GENERAL INFORMATION:

APPLICANT: IMClone Systems Incorporated, et al.

APPLICANT: IMClone Systems Incorporated, et al.

ITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR ITLE OF INVENTION:

INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 127;
Sequence 5, Application US/10374600
Publication No. US20030224001A1
GENERAL INPORMATION:
APPLICANT: IMCIONE Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                          ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: DCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
FLING DATE: CAPPLICATION VUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                          NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENČE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425-5288
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APPLICATION NUMBER: US/10/374,600
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SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-374-600-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6, 2004, 17:09:06
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDENDESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                        FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 QONNNWPTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October
Job time: 57.0526 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QQNNNWPTT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 MD storage
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: ECT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 127 amino acids; ; ; FYPE: amino acids; ; ; FYPE: amino acids; ; ; STRANDEDNESS: not relevant; ; MOLECTLE TYPE: peptide; ; ; FRAGENT TYPE: peptide; ; ; FRAGENT TYPE: internal; ; SEQUENCE DESCRIPTION; SEQ ID NO: 11: US-10-374-600-11.
                                                                                                                                                                                                                        CURRENT APPLICATION DABER: US/10/374,600
PRELICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Broadway CITY: New York
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: US
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Gaps
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PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C

FILING DATE: 19-Mar-1998

APPLICATION NUMBER: PCT/US6/09847

FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/482,982

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/573,289

FILING DATE: 15-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Deborah A. Somerville

REGISTRATION NUMBER: 31,995

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Sequence

Sequence Sequence

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RESULT 1
US-07-956-399-2
i Sequence 2, Application US/07956399
i Patent No. 5876717
i GENERAL INFORMATION:
APPLICANT: SHIMAWIRA, TOSHIRO
APPLICANT: HAWURO, JUNJI
ITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
ITLES OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
ITLES OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19221005
CLASSIFICATION: 530
US-08-436-463-21

US-09-436-463-18

US-09-339-92A-86

US-09-339-92A-86

US-08-955-53A-12

US-08-436-463-19

US-08-436-463-19

US-07-634-278-63

US-08-477-728-63

US-08-477-040-63

US-08-474-040-63

US-08-474-040-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-586-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5876717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELECOMUNICATION INFORMATION:
TELEPRAY: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 240 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8
Matches 7; Conservative
    ; MOLECULE TYPE: protein US-07-956-399-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O LIGMNNNOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                               TOPOLOGY:
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Appli
Appli
                                                                                                                                            October 6, 2004, 16:24:54 ; Search time 15.9474 Seconds (without alignments) 29:135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Ar
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Sequence 34,
Sequence 34,
Sequence 34,
Sequence 55,
Sequence 55,
Sequence 55,
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Sequence 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
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(GGDZ 6/ptodata/2/iaa/5B_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/5B_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-956-399-2
US-09-456-090A-84
US-07-634-278-34
US-08-477-728-34
US-08-477-728-34
US-08-477-728-34
US-08-477-728-34
US-08-478-17.65-55
US-08-476-17.65-55
US-08-476-17.65-4
US-08-476-17.68-4
US-08-476-17.68-4
US-08-476-17.68-4
US-08-476-17.68-4
US-08-476-17.68-4
US-08-476-17.68-6
US-08-477-17.68-6
US-08-477-17.68-6
US-08-477-17.68-6
US-08-477-17.68-6
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US-08-477-17.68-6
US-08-477-17.68-6
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                                                                                                                                                                                                                                                                                                                                                                                         389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                   US-09-635-974A-12
56
1 QONNNWPTT 9
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                     Title:
Perfect score:
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                                                                                                          OM protein
                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                                      Run on:
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Gaps

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Length 240; Indels

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TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                          Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-956-399-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                             90 QQTNTWPTT 98
                                                                                                                                                                        1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
TYPE: AMINO ACID
                                                                                                                                                                                                           원
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                                                                                  Sequence 84, Application US/09456090A

Sequence 84, Application US/09456090A

Patent No. 6680209

September No. 6680209

APPLICANT: Buechler, Joe

APPLICANT: Valkirs, Gunars

APPLICANT: Lonberg, Nils

TITLE OF INVENTION: HOWAN ANTIBODIES AS DIACNOSTIC REAGENTS

TITLE OF INVENTION: 1000000S

CURRENT REPLICATION NUMBER: US/09/456,090A

CURRENT FILICATION NUMBER: US/09/456,090A

CURRENT FILICATION NUMBER: US/09/456,090A

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 84

LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.6%; Score 44; DB 4; Length 224; Best Local Similarity 77.8%; Pred. No. 9.8; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1755 S. Jefferson Davis Highway, Suite 400° CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER EADBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFICATION: 530
ATTORNEY/ARCHION: 530
ATTORNEY/ARCHION: NO. 5876717man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10-586-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248955 OPAT UR
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT OTHER INFORMATION: M2-32L US-09-456-090A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 QQRNNWPLT 97
  90 QTNSWPTT 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
ADDRESSEE:
                                                       RESULT 2
US-09-456-090A-84
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US-07-956-399-4
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) LOCATION: 1..107

) OTHER INFORMATION: /note= "Amino acid sequence of the

CTHER INFORMATION: light chain for humane Lay antibody."

US-07-634-278-34
Score 44; DB 2; Length 239;
Pred. No. 9.4;
                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USITIOITING
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PULING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION:
                                                  0; Mismatches
                                                                                                                                                                                                                                                        5-07-634-278-34
Sequence 34, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
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Gaps
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                                                                                                                                                                                                                                                                                                              APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: COELINE, William P.
APPLICANT: COELINE, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTON: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: 379 Lytton Avenue
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..107

OTHER INFORMATION: /note= "Amino acid sequence of the OTHER INFORMATION: light chain for humane Lay antibody. US-08-474-040-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: REALBLE FORM disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 GURENT APPLICATION DATA: APPLICATION NUMBER: US/08/474,040 FILING DATE: 07-JUN-1995 CLASSIFICATION NUMBER: US/07/634,278 APPLICATION NUMBER: US 07/634,278 FILING DATE: 19-DEC-1990 APPLICATION NUMBER: US 07/530,274 FILING DATE: 13-PE-1990 PRIOR APPLICATION NUMBER: US 07/310,252 FILING DATE: 13-PE-1990 PRIOR APPLICATION NUMBER: US 07/310,252 FILING DATA: APPLICATION NUMBER: US 07/290,975 FILING DATE: 28-DEC-1989 PRIOR APPLICATION NUMBER: US 07/290,975 FILING DATE: 13-PE-1989 ATPORNEY/AGENT INFORMATION: NAME: Smith, William MREGISTRATION NUMBER: 30-233 REFERENCE/DOCKET NUMBER: 11823-002600 TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                    Sequence 34, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                     89 QQYNNWPPT 97
         1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                               RESULT 6
US-08-474-040-34
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                                                                                                                                                                                                                                                                                                                                         Patent No. 5585089
| GENERAL INFORMATION:
| APPLICANT: QUEEN, Cary L. |
| APPLICANT: GENERIDER, William P. |
| APPLICANT: SCHNEIDER, William P. |
| APPLICANT: SCHNEIDER, William P. |
| APPLICANT: SCHNEIDER, William P. |
| TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS |
| NUMBER OF SEQUENCES: 113 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Two meand and Townsend and Crew LLP |
| STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto |
| STATE: California |
| COUNTRY: US
      DB 1; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.0%; Score 42; DB 1; Length 107; Best Local Similarity 77.8%; Pred. No. 8.6; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
SOFTWARE: PATENTIN NATE: PATENTIN NATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
FILING DATE: 28-DE-1990
FILING DATE: 28-DEC-1990
FILING DATE: 28-DEC-1989
FILING DATE: 38-DEC-1989
FILING DATE: 38-DEC-19
                                                                     0; Mismatches
      Score 42;
Pred. No. 8
                                                                                                                                                                                                                                                                                                    Macour.
US-08-477-728-34
Sequence 34, Application US/08477728
Parent No. 5585089
      75.0%;
Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
LOCATION: 1..107
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                          89 QOYNNWPPT 97
                                                                                                                              1 QONNWWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-477-728-34
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89 QQYNNWPPT 97

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Gaps
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light chain for humane Lay antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 1; Length 107;
Pred. No. 8.6;
0; Mismatches 2; Indels
                                   Sequence 34, Application US/08487200
| Patent No. 5693762
| GENERAL INFORMATION:
| APPLICANT: CO, Man Sung
| APPLICANT: CO, Man Sung
| APPLICANT: COLINGH, Kathlem P. APPLICANT: COELINGH, Kathlem D. APPLICANT: SELICK, Marold B. TITLE OF INFORMINS.
| APPLICANT: MINIMAL PROPERTY SELICK, Marold B. TITLE OF INFORMION: IMPROVED HUMANIZED INFUNOGLOBLINS NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTER: CAILLOINIA
COUNTER: CAILLOINIA
COMPUTER READBALE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RC-DOS/MS-DOS
SOFTWARE: PACENTIN RC-DOS/MS-DOS
SOFTWARE: PACENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
RACK APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
RACK APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-ESP-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAMME: SMICKI, WILLIAM M
REGISTRATION NUMBER: 11823-002610
TELENCOMMUNICATION NUMBER: 11823-002610
TELENCOMMUNICATION NUMBER: 11823-002610
TELENCOMMUNICATION NUMBER: 11823-002610
                                                                                                                                                                                                                                                                                                                                    Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2420
INPORENTION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..107
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
RESULT 7
US-08-487-200-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-487-200-34
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LOCATION: 1..107
OTHER INFORMATION: /note= "Amino acid sequence of the
OTHER INFORMATION: light chain for humane Lay antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 42; DB 3; Length 107; 77.8%; Pred. No. 8.6; 2; Indels iive 0; Mismatches 2; Indels
                                     Sequence 34, Application US/08484537;
Patent No. (2180370)
PAPLICANT: CO. Man Sung
APPLICANT: LANDOLFI, William P.
APPLICANT: COELINGH, Wathleen L.
APPLICANT: ABDINGH, Wathleen L.
APPLICANT: MRESPONDENCE ADDRESS: 113
CORRESPONDENCE ADDRESS: 113
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PROOR APPLICATION DATA:
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 12-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 aming
                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 37
RESULT 8
US-08-484-537-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-484-537-34
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US-08-48-48-246A

Sequence 55, Application US/08485246A

Patent No. 6072035

GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES:
SEQUENCES:
ADDRESSE:
ADDRESSE:
No. 6072035artis Patent Department
STREET: S9 Route 10
CITY: East Hannover
STATE: New Jersey
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: Patent In Release #1.0, Version #1.25

COMPUTER: PatentIn Release #1.0, Version #1.25

STATE: PATENTION DATA:
FILING DATE:
FILING DATE:
FILING DATE: 27-SEPTEMBER-1993

APPLICATION NUMBER: US 07/952,802

FILING DATE: 27-SEPTEMBER-1993

APPLICATION NUMBER: 33,200

FRGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
COMPUTER READABLE FORM:
MEDIUM TYPS: Floppy disk
MEDIUM TYPS: Floppy disk
MEDIUM TYPS: Floppy disk
COMPUTER IBM PC compatible
COMPUTER STEEN PC COMPATIBLE
COMPUTER STEEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
FLING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY FAGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33.200
REFERENCE/POCKET NUMBER: 33.200
REFERENCE/POCKET NUMBER: 377-510
TELECOMMUNICATION INFORMATION:
TELECOMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 3;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (908) 277-4306
INPORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QONNNWPTT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-127-721A-55
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US-08-485-246A-55
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                                                             LOGATOR TO BE ADDICATION OF STANDARD OF SEQUENCE 55, ADDICATION US/08476176B

Patent No. 5958708

GENERAL INFORMATION:

APPLICANT: Saldanha, No. 5958708man

APPLICANT: Saldanha, Jose

TITLE OF INVENTION: Immunoglobulin isotype

TITLE OF INVENTION: Seshaped monoclonal antibodies against an ITILE OF INVENTION: Immunoglobulin isotype

NUMBER OF SOCIENCES: 55

CORRESSER: No. 5958708artis Patent Department

STREE: No. 5958708artis Patent Department

STREE: No. 5958708artis Patent Department

STREE: No. 5958708artis Patent Department

COMPUTRY: USA

SOFTWARE: No. 5958708artis Patent Department

COMPUTRY: IMP PC COMPATION

SOFTWARE: PATENT NO. 5958708artis Patent Department

COMPUTRY: USA

SOFTWARE: PATENT NO. 5958708artis PATENT

APPLICATION DATA: 88/17/721

FILING DATE: 27-SEPTEMBER-1992

APPLICATION NUMBER: US 07/952/28

FILING DATE: 25-SEPTEMBER-1992

APPLICATION NUMBER: US 07/952/28

FELIEPRONE: (908) 277-510

TELEPRONE: (908) 277-510
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| Sequence 55, Application US/08127721A
| Patent No. 6066718
| GENERAL INFORMATION:
| APPLICANT: Hardman, No. 6066718man
| APPLICANT: Kolbinger, Frank
| APPLICANT: Saladanha, Jose
| TITLE OF INVENTION: memunoglobulin isotype
| TITLE OF INVENTION: memunoglobulin isotype
| VORRESPONDENCE: 55
| CORRESPONDENCE: DESCRIPTION: Memunoglobulin isotype
| TITLE OF INVENTION: memunoglobulin isotyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 3e+05;
3; Mismatches 0; Indels
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                   JS-08-476-176B-55
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US-08-127-721A-55
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Gaps

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GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEGUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 3; Length 106;
Pred. No. 12;
3; Mismatches 0; Indels
                                                                                   Sequence 4, Application US/09296595A; Sequence 4, Application US/09296595A; Patent No. 612991S; GENERAL INFORMATION.
GENERAL INFORMATION:
APPLICANT: WILS, WINFRIED S.
APPLICANT: WILS, WINFRIED S.
APPLICANT: SCHNIDT, MATHIAS.
APPLICANT: SCHNIDER, DOUGLAS.
FILER REPERENCE: SCH-1576 D1.
CURRENT APPLICATION NUMBER: US/09/296,595A; CURRENT FILING DATE: 1999-04-23.
EARLIER APPLICATION NUMBER: 08/800,198
EARLIER APPLICATION NUMBER: 08/800,198
EARLIER PILING DATE: 1997-02-13.
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTESTONDENCESS:
CORRESPONDENCESS:
CORRESPONDENCESS:
STREET: 59 Route 10
CITY: Bast Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OF COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 07/952, 802
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952, 802
FILING DATE: 25-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708AK, Henry P.
REGISTRATION NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION NUMBER: 4-19276/A/P2/CIP
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Best Local Similarity 66.7
Matches 6; Conservative
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LENGTH: 106
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08800198;
Patent No. 5942602;
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: WAKALOPOULOU, EVANGELIA
APPLICANT: VAKALOPOULOU, EVANGELIA
APPLICANT: CHNBIDER, DOUGLAS;
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES;
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                           Query Match 73.2%; Score 41; DB 3; Length 9; Best Local Similarity 66.7%; Pred. No. 3e+05; Matches 6; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 18M PC compatible

COMPUTER: 18M PC compatible

COMPUTER: 18M PC compatible

CONFUNES: PatentIN PC-DOS/NS-DOS

SOUTHARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,198

FLING DATA: 13-FB-1997

CLASSIFICATION: DATA:

NAME: HAMLET AINO, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: SCH 1576

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TELNOFLOGY: linear

MOTECTIE TONE: Lanear

MOTECTIE TONE: Lanear
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMONIVICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acide
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Best Local Similarity 66.7
Matches 6; Conservative
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NO
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HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2200 CLA
                                                                                                                                                                                                                                                             US-08-485-246A-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-800-198-4
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(908) 277-5110 (908) 277-4306

89 QQSDSWPTT 97

Gaps

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Sequence 4, Application US/08127721A

Sequence 4, Application US/08127721A

Sequence 1 Rock 1 Recompany 100:

APPLICANT: Bardman, No. 6066718mn

APPLICANT: Saldanha, Jose

TITLE OF INVENTION: Feshaped monoclonal antibodies against an TITLE OF INVENTION: Seshaped monoclonal antibodies against an TITLE OF INVENTION: Memunoglobulin isotype

TITLE OF INVENTION: Seshaped monoclonal antibodies against an TITLE OF INVENTION: Memunoglobulin isotype

CORRESPONDENCE ADDRESS: 55

CORRESPONDENCE ADDRESS: 55

CORRESPONDENCE ADDRESS: 55

CONTUTRY: Bast Hanover

STATE: No. 6066718artis Patent and Trademark Department

STATE: Bast Hanover

STATE: May Jersey

COMPUTER: East Hanover

STATE: May Jersey

COMPUTER: EADBALE FORM:

MEMULICATION TRAJERSE 1993

COMPUTER: EADBALE FORM:

APPLICATION NUMBER: US/08/127,721A

FILING DATE: 2-SEPTEMBER-1993

FILING DATE: 2-SEPTEMBER-1993

FILING DATE: 2-SEPTEMBER-1993

FILING DATE: 2-SEPTEMBER-1993

FILING DATE: 3-SEPTEMBER-1993

FILING DATE: 3-SEPTEMB
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Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 0; Indels
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                                      SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66,7
Matches 6; Conservative
                                                                                                                                          TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-476-176B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MOLECULE TYPE: protein US-08-127-721A-4
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Search completed: October 6, 2004, 16:36:34 Job time : 16.9474 secs

89 QQSDSWPTT 97

1 QQNNNNWPTT 9

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	October 6, 2004, 16:20:48 ; Search time 45.4737 Seconds (without alignments) 55.921 Million cell updates/sec	US-09-635-974A-12 e: 56 .1 QONNIWPTT 9	e: BLOSUM62 Gapop 10.0 , Gapext 0.5	1586107 seqs, 282547505 residues	Total number of hits satisfying chosen parameters: 1586107
	OM protein - pr	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp21990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		e Liga	Aab37957 Anti-EGFR	Aau77789 Mouse lig	Kappa 1	Н	5 Kappa 1	941 Kappa	946 Kappa l	_	Single	Aaw05135 scFv(225)	40	σ	Aaw05141 scFv2 (FRP	σ	Aar34510 Fv(TU27).	9386	-	1511	Abr54897 Light cha	10	557	895	Abr54896 Light cha	Abr54891 Light cha
SUMMARIES	CI		AAYSSSIE	AAB37957	AAU77789	AAW08949 -	AAW08948	AAW08945	AAW08941	AAW08946	AAW08943	AAW05133	AAW05135	AAW05140	AAW05139	AAW05141	AAR32129	AAR34510	AAB99396	AAB75029	AAR34511	ABR54897	ABR54906	AAB69657	ABR54895	ABR54896	ABR54891
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	Score		ņ	26	26	56	99	56	56	56	56	56	56	56	26	26	45	45	44	44	44	43	43	42	42	42	42
	Result No.		-	7	m	4	ស	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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ABR54889 ABR54883 ABR54883 ABC61017 ADC61015 ADC99805 ADD05409	ADD05381 ADD13784 ADD13784 ADC61102 ADC61110 AMM77557 ABG59199 ABG46586 ABP45257 ABP45257 ABP45941
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## ALIGNMENTS

RESULT 1 AAY59316 ID AAY59316 standard; peptide; 9 AA. XX	AAY59316;	U/-MAK-ZUUU (IIISC ENCIY)	Light chain hypervariable region, CDR3.	Hypervariable region; complementar single chain antibody; growth inhibotoein receptor tyrosine kinase:	Min so.		XX PD · 25-NOV-1999.	XX PP 14-MAY-1999; 99WO-US010741.	XX PR 15-MAY-1998; 98US-00079612. PR 15-MAY-1998; 98US-0085613P. PR 07-DEC-1998; 98US-00206138.	XX. PA .(IMCL-) IMCLONE SYSTEMS INC. PA .(UABR-) UAB RES FOUND.	XX PI Waksal HW, Saleh MN, Robert F, Buchsbaum DJ;	A.A. WPI; 2000-062440/05. DR N-PSDB; AAZ48630.	XX Treatment of human tumors, using a combination of radiation and a non-PT radiolabeled protein receptor tyrosine kinase inhibitor.	XX PS Disclosure; Page 15; 31pp; English. VV			of tumours of e.g. breast, lung, colon, kidney, bladder,	AAY59316;  07-MAR-2000 (first entry) Light chain hypervariable region, CDR3. Hypervariable region; complementarity de single chain antibody; growth inhibitor; protein receptor tyrosine kinase; light Mus sp.  W09960023-Al.  15-MAY-1998; 98WS-00079612.  15-MAY-1998; 98WS-00056138.  15-MAY-1998; 98WS-00056138.  (MAZ-1998; 98WS-00056138.  (WARY-1998; 98WS-00056138.  The MAY-1998; 98WS-00056138.  (WARY-1998; 98WS-00056138.  Treatment of man tumors, using a combi radiolabeled protein receptor tyrosine k Disclosure; Page 15; 31pp; English.  This sequence is the hypervariable regiodetermining region 3) of the light channed erived from the murine antibody 225. The for inhibiting the growth of tumours in an effective amount of a combination of protein receptor tyrosine kinch can lead to tumourigenesis. The much can lead to tumourigenesis. The most tumours of e.g. breast, lung, colon,
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AAU77789 standard; peptide; 9 AA.

RESULT 3 AAU77789

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1 QONNNWPIT

(first entry)

05-JUN-2002

AAU77789;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-EGFR monoclonal antibody i chain V region CDR3 peptide sequence.
                                                                                                                                                                                                                  Gaps
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the patient makes the tumour more susceptible to radiotherapy
                                                                                                                                      100.0%; Score 56; DB 3; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB37957 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000; 2000WO-US011756.
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                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                           1 QONNNWPTT 9
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                                                                                                                                                 Query Match
Best Local Similarity
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                                                                        Sequence 9 AA;
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13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGF) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the antagonist and phototherapy. Chemotherapentic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal prosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic mammal with hyperproliferative disease such as psoriasis, actinic strandated by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 255 antibody light chain (LH) by pravious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for treating a mammal with
                                                                                                               Mouse, light chain; antibody; hyperproliferative disease; epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR3; EGFR inhibitor.
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                                                                                  Mouse light chain hypervariable region (CDR3) of 225 antibody.
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                                                                                                                                                                                                                                                                                                                                                     09-AUG-2000; 2000US-00635974.
                                                                                                                                                                                                                                                                                                                   09-AUG-2001; 2001WO-US041647.
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Best Local Similarity
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100.0%; Score 56; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 9; Conservative

AAW08949;

Homo sapiens

Key Region Region Region Region Region Region Region

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Kappa; light chain; reshaped; monoclonāl; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate variable region; framework; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
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                                                               Kappa light chain variable region of 225RA antibody.
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/label= CDR_2
57. .88
/label= framework_3
89. .97
/label= CDR_3
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85..49
/label= framework_2
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'label= framework 1
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/label= framework_4
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ID AAW08945 standard; protein; 127 AA.
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95US-00573289
                                (first entry)
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Les 9; Conserv
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                                                                                                                                                                                      Homo sapiens
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15-DEC-1995;
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Matches
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                                                                                            Kappa; light chain; reshaped; monoclonal; antibody; 225RB; human; pepidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostatic; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RA, The MAD is specific for the human epidermal prowth factor (BGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
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                                                           Kappa light chain variable region of 225RB antibody.
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/label= framework_2

/label= CDR_2

57. .88

/label= framework_3

89. .97

/label= CDR_3
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|label= framework_1
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95US-00573289.
                            (first entry)
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/label= (
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WPI; 1997-051897/05.

Goldstein NI,

07-JUN-1996;

07-JUN-1995; 15-DEC-1995;

WO9640210-A1

19-DEC-1996

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Query Match Best Local Similarity Matches 9; Conserv

Sequence 107 AA

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us-09-635-974a-12.rag

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Kappa, light chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                      Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the kappa light chain variable region of the murine monoclonal antibody (MAb) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells, especially conjugated to a cyctoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AUG-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kappa light chain variable region of 225RA antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                              Example IV; Fig 13; 112pp; English.
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95US-00573289.
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Best Local Similarity 100...
3, Conservative
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15-DEC-1995;
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15-DEC-1995;
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                                                                                                          Kappa; light chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric; L7'CL; leader sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the kappa light chain variable region of the chimeric monoclonal antibody (MAb) C225, with the modified leader sequence from the kappa light chain of L7.CL MAb. C225 is specific for the human epidermal growth factor (EGF) receptor. C225, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage special tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saldanha JW;
                                                                          Kappa light chain variable region of C225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example IV; Fig 17; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW08941 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT
                                                                                                                                                                                                                                                                                                                                                                              96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00482982
                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00573289
                                    18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 QONNNWPTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QQNNNNPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT49344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 127 AA;
                                                                                                                                                                                                            Mus; spp.
Homo sapiens.
                                                                                                                                                                                                                                                                                                      WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2003
18-SEP-1997
                                                                                                                                                                                                                                                                                                                                            19-DEC-1996,
                                                                                                                                                                                                                                              Synthetic.
    AAW08945;
                                                                                                                                                                                                                                                                    Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW08941;
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Matches

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Gaps

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Gaps

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EGF; therapy.

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scrv(225) (AAW05133) comprises the single-chain binding region of murine monoclonal antibody 225, which is specific for the human epidermal growth factor receptor. It is encoded by plasmid pWW152-225 (see also AAT42033), constructed by clonting MAD 225 whand VL region CDNAs into plasmid pWM152. Novel bivalent proteins (see also AAW05134-44), some of them including scFv(225) and an effector e.g. cytotoxin, can be produced in bacterial host cells, and are useful as antitumour agents
prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bivalent fusion proteins that bind epidermal growth factor receptor canalogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                  100.0%; Score 56; DB 2; Length 127
100.0%; Pred. No. 0.099;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Single chain antibody; scFv; monoclonal antibody; MAb; epidermal growth factor; receptor; antitumour; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .119
|label= VH_region
|note= "monoclonal antibody 225 VH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "monoclonal antibody 225 VL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "synthetic spacer peptide"
134. .240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                AAW05133 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 17; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                  Single chain antibody scFv(225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .20. .133
'label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-00106275.
                                                                                                                                                                                                                                                                                                        29-JAN-1997 (first entry)
                                                                       Query Match
Best Local Similarity 100.
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                                                                                                                                                                       109 QQNNNNPTT 117
                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wels W, Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-478748/48.
                                                                                                                                             1 QQNNNWPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT42033.
                                                         Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                        Mus; sp.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                           AAW05133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                  AAW05133
                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                              88888
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                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kappa; light chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the kappa light chain variable region of the chimeric monoclonal antibody (MAb) C225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - used
                                                           - nseq
                                                                                                                            The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (NAb) H325, 225RKA. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytocoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                        Gaps
                                                        Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tummour growth, esp. of late stage prostatic tummour.
                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                          100.0%; Score 56; DB 2; Length 127; 100.0%; Pred. No. 0.099; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kappa light chain variable region of C225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW08943 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example IV; Fig 15; 112pp; English.
                                                                                                  Claim 31; Fig 19; 112pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                        Similarity 100
9; Conservative
                                                                                                                                                                                                                                                                                                                                                               QONNWWPTT 117
                                                                                                                                                                                                                                                                                                                                  1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-051897/05.
N-PSDB; AAT49342.
               WPI; 1997-051897/05.
N-PSDB; AAT49345.
                                                                                                                                                                                                                                                Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spp.
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15-DEC-1995;
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Chimeric.
                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW08943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus;
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or

Sequence 240 AA;

Gaps

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Query Match 100.0%; Score 56; DB 2; Length 651; Best Local Similarity 100.0%; Pred. No. 0.55; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                              AAW05140 standard; protein; 892 AA.
                                                                                                269
                                                                         σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-478748/48.
                                                                                                                                                                                                                                     scFv2 (225/FRP5) -ETA
                                                                                                261 QONNWWPTT
                                                                         1 QONNNWPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT42040
Sequence 651 AA;
                                                                                                                                                                                                               29-JAN-1997
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                                                                                                                                                                                       AAW05140;
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                       RESULT 12
                                                                                                                                                    AAW05140
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scFv(225)-ETA (AAW05135) comprises the single-chain binding region (see also AAW05133) of murine monoclonal antibody 225, which is specific for human epidermal growth factor receptor, joined to exotoxin A (ETA). It is encoded by plasmid pSW202-225 (see also AAT42035) obtd. by ligating an scFv(225) gene (AAT42033) into plasmid pSW200 contg. the Pseudomonas enquinose PAK ETA gene. The construct can be used to produce novel bivalent fusion proteins (see also AAW05136-44) in bacterial host cells, for use as antitumour agents
                                                                                                                                                                                                                                                 Single chain antibody, scFv, monoclonal antibody, MAb, BGF, epidermal growth factor, receptor, plasmid pSW202-225, cancer, therapy, antitumour; exotoxin A, ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bivalent fusion proteins that bind epidermal growth factor receptor analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
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0
           100.0%; Score 56; DB 2; Length 240; 100.0%; Pred. No. 0.19;
                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "exotoxin A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                                                                             1. .21
/label= Sig peptide
/note= "ompA signal peptide"
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 19-20; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                AAW05135 standard; protein; 651 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          39. .278 |
|Jabel= scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANT-) SAN TUMORFORSCHUNGS GMBH
                                                                                                                                                                                                                                                                                                                                                                                                               22. .38
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                279. .289
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Groner B;
                                                                                                                                                                                                                         scFv(225)-ETA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-00106275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290. .651
/label= ETA
                                                                                                                                                                                                 (first entry)
                                     9; Conservative
                                                                                                                                                                                                                                                                                                    Mus sp.
Pseudomonas; aeruginosa.
                                                                          223 QQNNNWPTT 231
                                                           1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-478748/48
N-PSDB; AAT42035.
                       Local Similarity
                                                                                                                                                                                                29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1995;
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                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                          AAW05135;
                                                                                                                                                                                                                                                                                                                                        chimeric.
           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wels W,
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                         Best Loc
Matches
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Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                          Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-225-5; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                                                                                                                                                                                                /note= "endotoxin-A amino acids 380-613"
                                                                                                                                                                                                                                 990, .404<sup>-</sup>
|abel= ETA
'note= "exotoxin A amino acids 252-366"
                                                                                                                                                                   peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page 31-33; 52pp; English.
                                                                                                                                                    . . . 21
'label= Sig_peptide
'note= "ompA signal
                                                                                                                                           iocation/Qualifiers
                                                                                                                                                                                                                                                                                     SCFV (FRP5)
                                                                                                                                                                                              9. .278
label= scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                        (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                          405. .407
/label= Spacer
408. .647
/label= scFv(FR)
                                                                                                                                                                                                                                                                                                       /label= Spacer
659. .892
/label= ETA
                                                                                                                                                                            2. .38
label= Spacer
                                                                                                                                                                                                               79. .289
|abel= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                          Groner B;
                                                                                                                                                                                                                                                                                                                                                                                     95EP-00106275
                                                                                                                                                                                                                                                                                              548. .658
/label= Sp
                          (first entry)
                                                                                              Mus, sp.
Pseudomonas, aeruginosa.
Synthetic.
Chimeric.
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scFv2(225/FRP5)-BTA (AAW05140) comprises the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth actor receptor, see also AAW05133) joined to portions of exotoxin A from Pseudomonas acruginosa and to the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor exbB-2, see also AAW05134). It is encoded by plasmid pMS238-225-5 (AAY42040). This plasmid can be utilised in the prodn. of the bivalent fusion protein in bacterial (esp. E. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-5-225; cancer; exotoxin A; ETA; antitumour.
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                                                                                                                                                    100.0%; Score 56; DB 2; Length 892;
100.0%; Pred. No. 0.76;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Spacer
/label= Spacer
/label= Spacer
/label= ScFv(FRP5)
279. .289
/label= Spacer
290. .404
/label= ETA
/note= "exotoxin A amino acids 252-366"
/label= Spacer
/label= Spacer
/label= Spacer
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648. .658
/label= Spacer
659. .892
/label= ETA
/note= "endotoxin-A amino acids 380-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                    AAW05139 standard; protein; 892 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANT-) SAN TUMORFORSCHUNGS GMBH
                                                                                                                                                                                                                                                                                                                                                          scFv2(FRP5/225)-ETA (version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95EP-00106275.
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                     261 QQNNNWPTT 269
                                                                                                                                                                                                    σ
                                                                                                                                                                                                   1 CONNNWETT
                                                                                                                               Seguence 892 AA;
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                                                                                                                                                                                                                                                                                                             AAW05139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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scFv2(FRP5/225)-ETA (AAW05139) comprises the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor erbB-2, see also AAW05134) joined to portions of exotoxin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW05133). It is encoded by plasmid ppS238-5-225 (AAT42039). This plasmid can be utilised in the prodn. of the bivalent fusion protein in bacterial (sep. E. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                              Bivalent fusion proteins that bind epidermal growth factor receptor analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS240-5-225; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 56; DB 2; Length 892; 100.0%; Pred. No. 0.76; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acids 252-366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page 28-30; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW05141 standard; protein; 1020 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22. .38
/label= Spacer
39. .278
/label= scFv (FRP5)
279. .289
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Spacer
408. 647
/label= scrv(225)
648. 658
/label= Spacer
659. 1020
/label= ETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "exotoxin
05. .407
label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scFv2(FRP5/225)-ETA (version 2).
                      Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190. .404
| label = ETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638
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                      Schmidt M,
                                                                        WPI; 1996-478748/48.
N-PSDB; AAT42039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 QONNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 892 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW05141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                      Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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à
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Riethmueller G;

Kaluza B,

91DE-04143214. 91DE-04124759.

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This sequence is the light chain variable region of a preferred anti-IL2R beta monocolonal antibody for use in the claimed synergistic composition. The anti-IL2R beta antibody is used with at least one anti-CD4 antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See AAQ36607-Q36616. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                             Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-
                                                                      (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                   Claim 8; Page 17; 18pp; German.
                                                                                                        Scheuer W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October
Job time: 47.4737 secs
                                                                                                                                                                                                                               IL2R beta antibodies
                                                                                                                                            WPI; 1993-037582/05.
                                                                                                                                                             N-PSDB; AAQ36615
 30-DEC-1991;
                                  25-JUL-1991;
                                                                                                        Weidle U,
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                                                                                                                                                                                                                                                                                                                                                                                                          scFv2(FRPS/225)-ETA version 2 (AAW05141) comprises the single-chain binding region of murine monoclonal antibody FRPS (specific for human epidermal growth factor receptor erbB-2, see also AAW05134) joined to portions of exotoxin A from Fseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW05133). It is encoded by plasmid pMS240-5-225 (AAT42041). This plasmid can be utilised in the prodn. of the bivalent fusion protein in bacterial (esp. E. coli) host antitumour agents
                                                                                                                                                                                                                                                                                                   Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 56; DB 2; Length 1020; Best Local Similarity 100.0%; Pred. No. 0.88; Matches 9; Conservative 0; Mismatches 0; Indels (
 /note= "endotoxin-A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page 34-36; 52pp; English.
                                                                                                                                                                            (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                Groner B;
                                                                                                                                          95EP-00106275.
                                                                                                      95EP-00106275
                                                                                                                                                                                                              Schmidt M,
                                                                                                                                                                                                                                                  WPI; 1996-478748/48.
                                                                                                                                                                                                                                                                 N-PSDB; AAT42041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1020 AA;
                                                                                                      26-APR-1995;
                                                                                                                                          26-APR-1995;
                                  EP739984-A1
                                                                      30-0CT-1996
                                                                                                                                                                                                            Wels W,
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o,
                                                         Gaps
                                                         ..
O
                          Length 107;
                                                         1; Indels
                          Query Match 80.4%; Score 45; DB 2; Best Local Similarity 77.8%; Pred. No. 5.6; Matches 7; Conservative 1; Mismatches
                                                                                                                                                              6, 2004, 16:29:50
                                                                                                               97
                                                                                     9
                                                                                     1 OQNNNWPTT
                                                                                                        ||||:| ||
TTGWSNTQQ 68
Sequence 107 AA;
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immunosuppression; tissue transplantation; graft; L chain; V region; T-helper cell inhibition; transplant rejection; MAD; interleukin-2 receptor.

Location/Qualifiers

Homo sapiens

Region Region

1. .96 /label= V-region 97. .107 /label= J-region

DE4143214-A1

28-JAN-1993.

Anti-IL2R beta antibody MAb A41 light chain variable region.

(first entry)

(revised) (revised)

25-MAR-2003

AAR32129;

10-MAR-2003 02-JUN-1993

AAR32129 standard; protein; 107 AA.

RESULT 15 AAR32129

630 QQNNNWPTT 638

1 QONNNWPTT 9

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